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This 12.8 kb DNA sequence spans the region from -6.65 kb relative to the transcriptional start site to +6.15 (located in the third exon) of the murine endothelial growth factor (VEGF) receptor-2 gene for Fik-1. This portion of the Fik-1 gene was isolated from the liver of mouse strain 129/SvJ by screening a phage library of liver internation for the gene from the six significant he 5'-flanking region of the gene, in combination with sequences located within the first intron, specifically and reproducibly target expression of heterologous DNA to angloblasts during early stages of vascular equilatory sequences of the first intron also function as an autonomous endothelium specific enhancer when fused to a autonomous endothelium specific enhancer when fused to a neuron factors of the Ets and GATA families. The invention provides a new claimed recombinant DNA (I) comprising at least one regulatory sequence from an intron of the Fik-1 gene, or its homologue, to control expression in endothelial cells, in vivo, linked to (b) a
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these, or transformed cells, are used to identify agents (A), these, or transformed cells, are used to identify agents (A), these, or transformed cells, that suppress, activate or enhance transcription of genes in endothelial cells. (I), vectors and (A) are used to direct or prevent (for antisense sequences) expression of genes specifically in endothelial cells, e.g. for treating angiogenesis, cancer, diabetic retinopathy, rheumatoid arthritis etc., and in wound healing, particularly for treating vascular cisease (particularly proliferation of smooth muscle cells, specifically atherosclerosis), tumours and neuronal disorders. They may also be used to induce vascular disease in the transgenic animals or diagnostically, particularly for studying (mal)function, interactions and unregulated expression of endothelial products. (I) provide specific modulation of gene expression in endothelial
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ογ	841	cataatttgttggtctaggaataaacacactgtaagtttagaatcacggcccaaaca 900	
QQ	9176	gcataatttgttggtctaggaataaacacactgtaaagtttagaatcacggcccaaaca 923	Ñ
Qy Db	901	caagtetttaacaatgecaactagettetgagatteattaatgteatttaattaceatg 960 	īο
δ δ	96	Bttaattactaaatctatagttgtaacagcaacacatgtacatct 102	0 !
QΩ	25	ttaaaaaatatgtcattaattactaaatctatagttgtaacagcaacacatgtacatct 935	ហ
Sy Dp	1021 9356	89 ∹	0 5
P Q	1081	t 114 t 947	رة 0 ت
δ qq	1141	octeatettegtteaegtteae 120 	0 1
δλ	20	tattfgccaacaacgtcaatgccagctgagccttaggcagtcatctgtcttagcag 126	. 0
QQ	9536	tatttgcccaacaacgtcaatgccagctgaggccttaggagtcatctgttcttagtcag 959	ī.
QZ Dp	1261 9596	tattaattagttattettettettetgaga 132 	ري <u>ن</u>
Oy Dp	1321	38	0 2
SP G	1381 9716	a 144 977	0 5
oy Dp	1441	accatggtgggcatgttacaggttagttgactgaaaa 150 	0 5
oy Pa	1501 9836	tggtatgtatctctcaagatgcttttttgc 156 	0 5
ζ O	1561 9896	<pre>nagtctccagcttggtattggcatgagctcag 162 nagtctccagcttggtattggcatgagctcag 995</pre>	ō
å d	1621 9956	gttgggacccctagctattgctcattagacttacactatttta 168 	15
Oy Dp	1681 10016	gatatttttcttcc 174 	0 7
oy Op	1741	ctocatttaaatgtgctgtctttagaagccactgcctcagcttctgc 180 	3
oy Db	1801 10136	tacacagcatgataaaagacaatgggacggggtca 186 	0 6

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leukcyte; graft rejection; HIV infection; antinflammatory; wound repair; organ regeneration; asthma; arthritis; glomerulonephritis; cystic fibrosis; ulcerative colitis; Crohn's disease; multiple sclerosis; allergic encephalomyelitis; Altheimer's disease; coronary artery restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the coding sequence for Xenopus slit protein. The slit protein is useful for altering or guiding cell migration of neural
                                                                                                                    10375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New vertebrate DNA encoding a slit protein that is useful for treating graft rejection, inhibiting infection of a cell by human immunodeficiency virus, inhibiting inflammation, and for aiding wound repair and organ regeneration.
  cagiggetecegtecetiteaggggialgagagaegagetgiagagagagatgieteceaggga 1920
                                                                                                                                                                                                                                                                                                                                                                                               frog; cell migration; neuronal; nerve axon; dendrite;
                                                                             gttttcattaatcagcaatttagtcagatctgtgcatcctatgctttacaagaaatgtca
                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                C63529 standard; DNA; 5513 BP
                                                                                                                                                                                                                                                                                                                                                                           Slit protein coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 72pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu JY;
                                                                                                                                                                                                                                                                                                                                                                                               Slit protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001
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C63529/c
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cells preferably nerve axons or dendrites, leukocytes or malignant cells expressing roundabout (robo) protein, by repulsion or inhibition. Also, the slit protein is useful for treating graft rejection, inhibiting the infection of a cell by HIV, inhibiting inflammation and in aiding wound for the treatment of conditions involving the migration of leukocytes, such as asthma, arthritis, glomerulonephritis, cystic fibrosis, ulcerative colitis, Crohn's disease, multiple sclerosis, allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piwi family nucleic acids, polypeptides, and antibodies, useful in gene therapy of diseases such as cancer and in various research and
                                                                                                                                                                                                                                                                                                                                       1653 attgctcattagacttacactatttttagttttgctctgagtttatgaatatgcatgtat 1712
                                                                                                                                                                                                                                                                                                                                                                    4054 TITGTICACAAAATITACGCTGACTAGTITITCACATITGTTTCCACGATAGCCAGGCAG 3995
                                                                                                                                                                                                                                                                          ctccagcttggtattggcatgagctcagagctttgattaatgagttgggaccccctagct 1652
                                                                                                                                                                                                                                                                                                      4114 CTGCAGAGTGATGTTGGCCTGAGCGCGGATCTTTGTCGAAGGAATTGGGGATAAACGAGTC 4055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ily protein; piwi; miwi; hiwi; gene therapy; tissue dystrophy; immunodeficiency; male infertility; mouse; ds.
                                                                                                                              encephalomyelitis, Alzheimer's disease and coronary artery restenosis.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    1713 gcatgaacttgggagatatttttcttccccaattcctttcctccatttaaatgtgc 1769
                                                                                                                                                                                                                                                                                                                                                                                                                    3994 GCACTGGCACAGAACATTCCCTTTCACAATGCATTGGGCTCCATTTTGACATTC 3938
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                                                                                                                                                                                                               Length 5513;
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/product= miwi
/product= miwi
/transl_except= (pos:450..452; aa:Xaa)
/transl_except= (pos:1337..1339; aa:Xaa)
/rote= "Xaa= Leu or Ile"
/rote= "Xaa= Leu or Ile"
/note= "Xaa= unspecified amino acid"
                                                                                                                                                             Sequence 5513 BP; 1668 A; 1216 C; 1211 G; 1418 T; 0 other;
                                                                                                                                                                                                          Score 55.4; DB 21;
Pred. No. 3.6e-05;
); Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse piwi gene, designated miwi.
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ilarity 57.1%;
Conservative (
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                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piwi family
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                                                                                                                                                                                                                                         Matches 101;
                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anaemia;
                                                                                                                                                                                                                            Local
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                                                                     miwi. The piwi family nucleic acids and polypeptides are used in gene therapy of diseases such as cancer and also in various research and diagnostic applications. The sequences can also be used to treat
                                                                                                                                                                                                                                                   1298 ttagttattettettettgagacagagteteaetgtgtgggeecaggetagteteaaaet 1357
                                                                                                                                                                                                                                                                               3656 TICTTTTTTTTTTTGTTTAAGACAAAGTCTCACTATGTAGCCTAGGCTGACCGGGAACT 3597
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding the WRN gene product useful for detection and treatment of Werner's syndrome, and related
                                                                                                                   tissue dystrophy, anaemia, immunodeficiency, and male infertility.
                                                         This sequence encodes the mouse piwi family protein, designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Werner's syndrome; detection; diagnosis; autosomal; isorder; phenotype; ss.
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                                                                                                                                                 Sequence 4064 BP; 1114 A; 978 C; 1077 G; 890 T; 5 other;
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                                                                                                                                                                                                          0.014;
                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                          2.0%; Score 46; 63.6%; Pred. No.
                          Claim 19; Page 180-185; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Partial mouse WRN genomic sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 7; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  X83007 standard; DNA; 51259 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recessive disorder; phenotype;
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95US-0580539.
96US-0010835.
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diagnostic applications
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Matches 70; Conserv
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OSHIMA J.
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29-DEC-1995;
30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WRN;
                                                                                                                                                                                            Query Match
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0; Gaps

DB 21; Length 2362; 0.019; 25; Indels

Score 45; DB 2: Pred. No. 0.019; 0; Mismatches

2.0%;

Query Match 2.0% Best Local Similarity 70.6% Matches 60; Conservative

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1280 atgoctgoctgctattaattagttattcttctcttgagacagagtctcactgtgtggc 1339

1727 CCAGGCTGGTCTCAAACTCCCGGCC 1703

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V29343 standard; DNA; 1110

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V29343/c RESULT

1340 ccaggetagteteaaacttgeggte 1364

is an mRNA encoding a homologue of human tTGase, expressed in LTR-HPC

Sequence 2362 BP; 616 A; 593 C; 640 G; 513 T; 0 other;

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                                                                                                                                                                                                            Db 23743 ttttagttttagttttactttttttttagacagggtctcactgtgtagctgggacaagct 23802
                                                                                                                                                                            1292 tattaattagttattcttctctctgagacagagtctcactgtgtggcccaggctagtct 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Human tissue transglutaminase homologue-3"
/note= "GTP binding calcium dependent enzyme"
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                        Db 23803 ccaccctgttccccttttcctcacctcctgagtgctgggatcacaggcgtgtgc 23858
                                                                                                                                                                                                                                                                                1352 caaacttgcggtccatttgtctcactcatcagaatgctgggcttccaggtgtgtgc 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruman tissue transglutaminase (tTGase) homologue-3 encoding mRNA.
                                                                                                                           ó
                                                                           Length 51259;
Sequence 51259 BP; 14533 A; 9635 C; 10266 G; 16825 T; 0 other;
                                                                                                                           44; Indels
                                                                        Score 45.6; DB 18;
Pred. No. 0.069;
                                                                                                                           0; Mismatches
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133..1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z50462 standard; mRNA; 2362 BP
                                                                        2.0%;
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/product=
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                                                                                                   Best Local Similarity 62.1 Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
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                                                                           Query Match
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Calcium ion channel alphal subunit exon 15/intron partial sequence.

(first entry)

31-JUL-1998

V29343;

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intronic sequences containing the complete coding region of the human calcium ion channel alpha 1 subunit gene and part of untranslated sequences. The channel is related to familial hemiplegic migraine (FHM) and/or episodic ataxia type 2 (EA-2) and is derived from, related to or associated with a gene present in humans on chromosome 19p13.1-13.2. The encoding gene can be used to localise or identify genes related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences shown in V29330 to V29371 represent the 47 exons and flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human nucleic acid associated with migraine and episodic ataxia type 2\, - useful for diagnosis and development of specific treatments
                                                               Calcium ion channel alphal subunit; human; episodic ataxia type 2; familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Terwindt GM:
                                                                                                                                                                                /number= 14
/note= "partial sequence"
202..274
                                                                                                                                                                                                                                                                            /number= 15
/note= "partial sequence"
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                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      96EP-0202707
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                                                                                                                                                                                                                                      /number= 15
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                                                                                           exon; intron; ss.
                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      27-SEP-1996;
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repopulating haematopoietic progenitor cells (LTR-HPC), by comparing the expression of tissue transglutaminase (tTGase), a calcium dependent enzyme, in myeloid cells like blood or marrow to a standard. A higher level of tTGase expression, indicates the presence of LTR-HPC in the sample. Tissue TGase catalyses post-translational modification of proteins and is involved in appotosis, cell adhesion, metastasis and extracellular matrix (ECM) assembly. It acts as a marker that distinguishes the LTR-HPC from other (im)mature blood cells and is also useful for improved quantification of a mammal's haematopoietic competence. The method is useful for functional selection of progenitor cells, enabling allogeneic transplant procedures and ex vivo manipulation of HPC for use in gene therapy. The present sequence

The patent discloses a method of differentially identifying long-term

Disclosure; Page 48-50; 59pp; English.

Differentially identifying long-term repopulating hematopoietic progenitor cells using tissue transglutaminase, useful for improving medical procedures, including gene therapy

Visser JWM, Ivanova NB; WPI; 2000-195317/17. P-PSDB; Y44919.

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episodic neurological disorders, specifically migraine, FHM or EA-2, but also epilepsy. The isolated or a recombinant nucleic acid can also be used to distinguish between alleles of the corresponding gene. Cells and animals containing recombinant expression vectors comprising the nucleic acid can be useful in study, development and treatment of migraine, FHM, EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and natural or synthetic antibodies against the proteins can be used to diagnose FHM, EA-2, migraine and other neurological conditions associated with cation channel disfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a library of human polynucleotides comprising the sequences given in 212532 to 217779. Also described is a method of detecting differentially expressed genes correlated with the
                                                                                                                                                                                                                                                                                                        1287 cctgctattaattagttattcttctcttctgagacagagtctcactgtgtgggcccaggct 1346
                                                                                                                                                                                                                                                                                                                              939 CCAGCTAATTATTATTATTTTTTTTTTTGCAGAGACGGAGTCTCACTATGTTGCCCAGACT 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, gene, gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profilling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
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                                                                                                                                                                                                                                       DB 19; Length 1110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene expression product cDNA sequence SEQ ID NO:3965.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA,
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                              Sequence 1110 BP; 306 A; 287 C; 275 G; 239 T; 3 other;
                                                                                                                                                                                                                                1.9%; Score 44; DB 19
71.8%; Pred. No. 0.025;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1883; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216495 standard; cDNA; 810 BP.
                                                                                                                                                                                                                                                                                                                                                                             1347 agtctcaaacttgcggtc 1364
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98US-0072910.
98US-0075954.
98US-0080114.
                                                                                                                                                                                                                                                                                                                                                                                                              879 TGTCTCAAACTCCTGGCC 862
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crkven, Garce
Escobedo J, Garce
Jones WL, Kassam A, P
Leshkowitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-494092/41.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09938972-A2.
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31-MAR-1998;
03-APR-1998;
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cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in 212532 to 217779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, itssue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as diagnosis, prognosis and management of colorectal cancer, breast cancer, papiling analysises and antanomic can also be used to screen for partial analysis and analysis can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition; interleukin-1 receptór; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1293 attaattagttattettetettetgagacagagteteactgtgtgggeecaggetagtete 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding the new human cytokine Tango-77 used to inhibit inflammation and to screen for specific modulators \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 810;
                                                                                                                                                                                                                                                                                                                                                                             Sequence 810 BP; 256 A; 145 C; 148 G; 253 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9%; Score 43.6; DB 2
64.3%; Pred. No. 0.027;
Live 0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                       peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537 gccagg 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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Best Local S
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                                                                                       X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-1ra. Such fragments are used in the method of the invention which describes the isolation of a novel human TRNGO-77 encoding nucleic acid and protein. Tango-77 is a member of the cytokine superfamily that is expected to inhibit inflammation by binding to the interleukin-1 receptor (IL-1R). It may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo A1; low density lipoprotein; LDL; blood; therapy; atherosclerosis; high density lipoprotein; HDL; cholesterol; coronary heart disease; Alzheimer's disease; hypobetalipoproteinemia; dysbetalipoproteinemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo E; Apo B; hyperlipidemia; human; treatment; hepatocyte; apoprotein; Apo Al; low density lipoprotein; LDL; blood; therapy; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1261 tgcgaattagaaagcctggatgcctgcctattaattagttattcttcttcttgaga 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel method for the genetic treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 43.2; DB 20; Length 11901; 63.5%; Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Indels
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(YESH ) UNIV YESHIVA BINSTEIN COLLEGE.
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                             Example 5; Figure 3; 226pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Apo Al genomic DNA.
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hyperlipidemia by altering genes, in hepatocytes, for apoprotein (apo) B, E or Al. Low density lipoprotein (LDL) levels in the blood are reduced by altering an apo B gene (I) in a hepatocyte. The invention describes a method for the therapeutic and/or prophylactic method involving altering an apo B gene in hepatocytes by introducing the mutations Argli2Cys, Argl5Gys or Cysl5BArg and a method for ameliorating atherosclerosis by altering the apo Al gene in a hepatocyte so that the altered protein can dimerize. Altering expression of apo genes regulates levels of high and low density lipoprotein cholesterol. Altering expression of apo B, E and Al genes is used to treat or prevent atherosclerosis, coronary heart disease, Alzheimer's disease, hypobetalipoproteinmia, and dysbetalipoproteinmia. This sequence encodes the human Apo Al protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1310 ctcttctgagacagagtctcactgtgtggcccaggctagtctcaaacttgcggtccattt 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3414 TTTAGTAGAGACAGGGTTTCACCATATTGGCCAGGCTGGTCTCAAACTCCTGGCCCTGAA 3355
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8966 BP; 2045 A; 2581 C; 2645 G; 1693 T; 2 other;
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Pred. No. 0.19;
0; Mismatches 54;
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/note= "EASE (Claim 1)"
5980..14507
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/note= "EASE (Claim 1)"
8671..10515
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note= "EASE (Claim 1)"
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/note= "EASE (Claim 1)"
14290..14507
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/note= "EASE (Claim 1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..14507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T73568 standard; DNA; 14507 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "EASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.9%;
Best Local Similarity 58.1%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0100..14923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cricetulus sp
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misc_feature

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1348 gictcaaact-igcggiccatitgictcactcatcagaaigcigggciiccaggigigig 1406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 tecaggaaetecagagatecacetgeetectgetteetgagtgetgggattaaaggtgtgtg 265
                                                                                                                                                                                                                                                                                                                        Expression augmenting sequence elements - used in vectors for expressing recombinant proteins at high levels in shorter periods of
                                                                                                                                                                                                                                                                                                                                                                                                                        A 14507 bp DNA sequence (T73568) comprises a novel transcription regulatory element, expression augmenting sequence element (EASE), that facilitates high expression of recombinant proteins in mammalian host cells. It was identified by cloning the integration site of a unique expression cassette encoding recombinant dimeric tumour necrosis factor receptor immunoglobulin Fc fusion protein from genomic DNA of a CHO 2AS-3 cell line expressing this protein at a high level. Expression vectors incorporating an EASE show a 2-to 8-fold improvement of recombinant protein expression levels in CHO host cells. The EASE sequence also facilitates high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EASE; expression augmenting sequence element; chinese hamster; ds.
            "the EASE sequence is preferably ligated to DNA comprising nucleotides 14290-14507 (Claim 3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.9%; Score 42.2; DB 18; Length 14507; 59.9%; Pred. No. 0.32; Live 0; Mismatches 58; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14507 BP; 4225 A; 2548 C; 3136 G; 4598 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression in shorter periods of time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chinese hamster 2A5-3 lambda EASE DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 ctgactacaggcaagcttgtttgttta 292
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 23-30; 36pp; English.
                                                                                                                                                                                                                                                        Thomas JN;
                                                                                                                                                     97WO-US00483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z88869 standard; DNA; 14507
                                                                                                                                                                                     96US-0586509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
/*tag~
/note=
                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                          WPI; 1997-372861/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 88; Conserv
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                                                                                   WO9725420-A1
                                                                                                                                                   10-JAN-1997;
                                                                                                                                                                                     11-JAN-1996;
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This invention describes a novel expression augmenting sequence element (EASP) (1) isolated from Chinese hamster ovary cells. (1) facilitates high expression of recombinant proteins in mammalian host cells in a short time period. (1) is used for improving expression of recombinant proteins 2-8 fold in stable cell pools when it is present in an expression vector. (1) improves recombinant protein expression in mammalian cells and facilitates the use of mammalian cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; prevention; treatment; protein therapy; agene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; foctal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; alleray; asthma; sepsis; diabetes; AIDS; Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1348 gtctcaaaact-tgcggtccatttgtctcactcatcagaatgctgggcttccaggtgtgtg 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1288 ctgctattaattagttattcttctctctgagacagagtctcactgtgtgggcccaggcta 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Improved expression of recombinant proteins in stable cell pools of mammalian cells comprises transforming cells with a vector containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.9%; Score 42.2; DB 21; Length 14507; 59.9%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14507 BP; 4225 A; 2548 C; 3136 G; 4598 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein cDNA fragment containing gene 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                          an expression augmenting sequence element -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1407 caccacactaggtagctcgcgttttaa 1433
                                                                                                                                                                                                                                                                             Claim 1; Column 17-30; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctgactacaggcaagcttgtttgttta 292
                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant protein production.
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                                  97US-0785150
                                                                  96US-0586509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88; Conservative
                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                      WPI; 2000-194831/17.
                                13-JAN-1997;
                                                                  11-JAN-1996;
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22-FEB-2000
                                                                                                                                        Morris AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                     This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polypucleotides. Specific uses are absence of mutations in the new polypucleotides specific uses are described for each of the 70 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, asthma, sepsis, diabetes, Alzheimer's and cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine disorders, infections and AIDS: The human secreted proteins of the invention are represented in X07744-Y07860 and the encoding nucleic acids are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                 New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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0
                                                                                                                                                                    Feng P;
Lafleur DW;
Shi Y, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer antigen nucleotide sequence SEQ ID NO:188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 687 BP; 187 A; 148 C; 161 G; 187 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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Pred. No. 0.07;
0; Mismatches
                                                                                                                                                                   R, Endress GA,
Komatsoulis GA,
n CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                   Claim 1a; Page 226-227; 280pp; English.
                                                                                                                                                                             Florence KA, Komats
sen HS, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1343 ggctagtctcaaacttgcggtc 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGGTCTCAAACTCTAGGGC 589
                                                                                                                                                                      Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C98178 standard; cDNA; 833 BP
                    970S-0056368
970S-0056369
970S-0056335
970S-0056555
970S-0056556
970S-005628
970S-005628
                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%;
Similarity 69.5%;
                                                                                                                      97US-0056728
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                                                                                                                                                                                           Olsen HS,
                                                                                                                                                                    Duan R,
                                                                                                                                                                                                                                WPI; 1999-190160/16.
                                                                                                                                                                                                                                           P-PSDB; Y07808.
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                                                                                                                                                                                Florence C,
Moore PA, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
                                                         19-AUG-1997
19-AUG-1997
                                               19-AUG-1997
                                                                                 19-AUG-1997
                                                                                               19-AUG-1997
                                                                                                         19-AUG-1997
                                                                                                                                                                    Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S.
Matches 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C98178;
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C97991 to C98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in B53234 to B54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antilnfective and antibacterial activities, are no be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1267 ttagaaagcctggatgcctgcctgctattaattagttattcttcttcttctgagacagagt 1326
                 identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; reproductive disorder; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 0.089;
0; Mismatches 28;
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue, cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphom; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens

WO9839448-A2

11-SEP-1998

06-MAR-1998;

9705-0038621 9705-0038621 9705-0040163. 9705-0040163. 9705-0040334. 9705-0040331. 9705-0040331. 9705-0040331. 9705-0043313. 9705-0043313. 9705-0043313. 9705-0043313. 9705-0043569. 9705-0043569. 9705-0043569. 9705-0047592. 9705-0047581. 9705-0047581. 9705-0047581. 9705-0047582. 9705-0047583. 9705-0047613.

1997; 997;

997; 997; I-APR-

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1997: 997 997 MAY -] 3-MAY-

MAY - 1 MAY-

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MAY-1997

23-MAY-1997

9705-0047633. 9705-0048964. 9705-00489610. 9705-0049610. 9705-0051926. 9705-0055274. 9705-005630. 9705-0056630. 9705-0056630. 9705-0056630. 9705-0056630. 9705-005664. 9705-005664. 13 - JUN - 1997; 08 - JUL - 1997; 16 - JUL - 1997; 18 - AUG - 1997; 22 - AUG - 1997; 22 - AUG - 1997; 22 - AUG - 1997; 22-AUG-1997

22-AUG-1997; 22-AUG-1997; 22-AUG-1997, 22-AUG-1997,

997

97US-0056872. 97US-0056874. 97US-0056875. 1997; 1997; 1997; 22-AUG-1997 22-AUG-1997 22-AUG-1997 22-AUG-1 22-AUG-1

97US-0056876. 97US-0056877. 97US-0056878. 97US-0056879. 97US-0056880. 97US-0056881. 97US-0056882. 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 166 266 22-AUG-1997 22-AUG-

970S-0056886. 970S-0056886. 970S-0056887. 970S-0056889. 970S-0056899. 1997; 1997; 1997; 997; 1997 22-AUG-1 22-AUG-22 - AUG - . 22-AUG-

1997; 22-AUG-22-AUG-1

97US-0056894. 97US-0056903. 97US-0056908. 22-AUG-1997 22-AUG-1997

97US-0056910. 97US-0056911. 97US-0057650. 97us-0056909 05-SEP-1997

(HUMA-) HUMAN GENOME SCI INC.

Ebner R, Endress GA; Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS; Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA; Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;

WPI; 1998-506364/43. P-PSDB; W74830.

New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 333-334; 721pp; English.

This sequence represents a nucleic acid molecule designated Gene 101 from the human cDNA clone HLQAB52 (deposited as clone ATCC 97901 and ATCC 209047) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. V59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions and be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides.

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Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V59511 for described
                                                                      0; Gaps
                                                                                                                                                                                                 Human; purH; biallelic marker; single nucleotide polymorphism; SNP;
diagnosis; prevention; treatment; prostate cancer; tumour;
chromosome 1q34-q35; ds.
                                             Query Match
1.8%; Score 41.8; DB 19; Length 1751;
Best Local Similarity 61.5%; Pred. No. 0.13;
Matches 67; Conservative 0; Mismatches 42; Indels 0;
                                                                                                         1690 GCGGACTGCAGTGCCGCAATCTCGCTCACTCCCGCTTCCCGG 1642
                                                                                                 1352 caaacttgcggtccatttgtctcactcatcagaatgctgggcttccagg 1400
                                                           42; Indels
                           Sequence 1751 BP; 405 A; 477 C; 476 G; 393 T; 0 other;
                                                                                                                                                                                      Human purH gene genomic DNA sequence.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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47: em_ph::*

48: em_aph::*

48: em_aph::*

48: em_aph::*

51: em_un::*

52: em_ap::*

53: gp_ats::*

54: gp_ats::*

55: gp_ats::*

56: gp_htg::*

60: gp_htg::*

61: gp_htg::*

62: gp_htg::*

63: gp_htg::*

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65: gp_htg::*

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66: gp_htg::*

67: gp_htg::*

68: gp_htg::*

69: gp_htg:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AX002124 Sequence	AF061804 Mus muscu	AF153058 Mus muscu	AC021220 Homo sapi	AC019251 Homo sapi	AC013745 Homo sapi	AC016982 Mus muscu	AF088189 Mus muscu
	ID	AX002124	AF061804	AF153058	AC021220	AC019251	AC013745	AC016982	AF088189
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0; Mismatches

Query Match 100.0%; Score 2273; Best Local Similarity 100.0%; Pred. No. 0; Matches 2273; Conservative 0; Mismatches

Length 12845; Indels tctcgagacagagccgctgttgttttccttctggtctttgagcgggaaggataacagtg 60

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Rappel,A., Ronicke,V., Damert,A., Flamme,I., Risau,W. and Breier,G.
Identification of vascular endothellal growth factor (VBGF)
receptor-2 (Fik-1) promoter/enhancer sequences sufficient for
angloblast and endothelial cell-specific transcription in
                                                                                                                                                                                         Mus musculus
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 510)
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Submitted (28-APR-1998) Molekulare Zellbiologie, Max Planck
Institut fuer physiologische und Klinische Forschung, Parkstrasse
1, Bad Nauheim 61231, Germany
Location/Qualifiers
                                                                                        AF061804 510 bp DNA ROD 23-AUG-1999
Mus musculus fetal liver kinase l (Flkl) gene, intronic enhancer.
AF061804
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    /organism="Mus musculus"
    /strain="C57BL"

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/gene="Flk1"
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2 (bases 1 to 430)

Kappel,A., Risau,W. and Breier,G.

Direct Submission
Submitted (21-MAY-1999) Molecular Cell Biology, Max-Planck,
Institut fuer Physiologische und Klinische Forschung, Parkstrasse
1, Bad Nauheim 61231, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kappel, A., Risau, W. and Breier, G. Prerequisite role of SCL/tal-1, GATA and Ets transcription factor binding sites for the in vivo function of Flk-1 gene regulatory
                                                                                                2181 aagtcaatcccacctttatacaatgaattgctgaagaggccttttaaaaacttggagtgtg 2240
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                              1822 ctggtacacagocatgataaaagacaatgggacggggtcacagtggctcccgtcccttca 1881
301 CAGGAAAACAGGAACTCCACCCTGGTGCCGTGAATTGCAGAGCTGTTGTTGTTGTG 360
                                                                                                                     121 GGGGTATGGAGACGAGCTGTAGAGAGATGTCTCCAGGGAGTTTTCATTAATCAGCAATTT 180
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Mus musculus tyrosine kinase FLK-1 minimal enhancer sequence.
AF153058
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                                                                                                                                                                                 481 CATTGTTTATGGAAGGCTTTCCTATTGGA 510
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1. .430
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Best Local Similarity 100.0
Matches 430; Conservative
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Direct Submission Submission Submitted (15-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mn 63108, USA On Nov 15, 2000 this sequence version replaced 91:9309528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 214348)
Waterston,R.H.
                                              241 GGAGGTTCATCGGGTTTCAATGTCCCGTATCCTTTTGTAAGACCTTGAAGTTGGCAACGC 300
                                                                                                                                                      AC021220 214348 bp DNA HTG 15-NOV-2000 HOMO sapiens chromosome 4 clone RP11-530117, WORKING DRAFT SEQUENCE, 38 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; 13% Sequencing vector: plasmid; 13% of reads Chemistry: Dye-primer ET; 87% of reads Chemistry: Dye-terminator Big Dye; 13% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 195065 bases at least Q40
Consensus quality: 200600 bases at least Q20
Consensus quality: 203756 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 210648; sum-of-contigs
Quality coverage: 4.62 in Q20 bases; sum-of-contigs
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1684: gap of unknown length
4194: contig of 2510 bp in length
4294: gap of unknown length
6424: contig of 2130 bp in length
6524: gap of unknown length
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
                                                                                                                                                                                                                                                                2182 agtcaatccc 2191
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f unknown length
g of 16469 bp in length
f unknown length
g of 22038 bp in length
f unknown length
g of 24422 bp in length
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g of 1231 bp in length
f unknown length
g of 1145 bp in length
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of 1055 bp in length
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of 9967 bp in length
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of 9080 bp in length
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gap of unknown length
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of 1100 bp in length
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208803: contig of 2027 bp
208903: gap of unknown le
210597: contig of 1694 bp
210697: gap of unknown le
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/note="assembly_name:Contigll1"
104898. .129319
/note="assembly_name:Contigll2
clone_end:SP6
/chromosome="4"
/clone="RP11-530117"
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Shiren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boduslavkiy, L., Baldwin, C., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Galegan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135552)
                                                                                                                                                      Db 100808 AGTATATTAATATGCATGTATGTGTGGAATTGGGGAATGTTTTCTCTTCCTCAGTTTCTC 100749
                                                                                                                                                                                                                                                                        Db 100748 TCCCTTGCTTTTAATGTACAGTCTTTATGAGCCATTATTATGAGCTGTGGCAGTTTGGTTA 100689
                                                                                                                                                                                                                                                                                                                                                                     DD 100688 CCAGGGGAAGCGCACTAGA-AAATTGATAAAGGAAAATGAGACAAGGTCATAGATTCTCT 100630
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                                                                                                                                                                                                                 1751 ttcctccatttaaatgtgctgtctttagaagccactgcctcagcttctgcagctcagata 1810
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                                                                                            1692 agtttatgaatatgcatgtatgcatgaacttgggaatatttt-tcttccccaattcctt 1750
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         Pred. No. 4.4e-73;
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   78.4%;
Best Local Similarity 78.4 Matches 468; Conservative
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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Zimmer, A. and Zody, M.

Limmer, A. and Zody, M.

John Street, Cambridge, MA 02141, USA

On Mar 5, 2000 this sequence version replaced gi:6649482.

All repeats were identified using RepeatMasker:

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This record contains 153 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the record is updated, the accession number will
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if 767 bp in length
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14758: contig of 732 bp in length
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Web site: http://www-seq.wi.mit.edu
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Sharen, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Bogualavkiy, L., Boukigalter, B., Brown, A., Castle, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Castle, A., Castle, A., Colangelo, M., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fizhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehockky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, H., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Direct Submission

Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

O'Jul 13, 2000 this sequence version replaced gi:6910837.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker:html
                               Homo sapiens chromosome 4 clone RP11-92P18 map 4, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 126330)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 4, clone RP11-92P18

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contra ~ 100 bp contig of 691 bp in length of 100 bp antig of 736 bp in length contig of 736 bp in length
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contig of 737 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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                                                                                                 AC013745
AC013745.3 GI:9114527
HTG; HTGS_PHASE0.
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4840:
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34 17333; gap of 100 bp 11 length 18057; contig of 724 bp in length 18058; contig of 724 bp in length 100 bp 18157; gap of 100 bp 100 bp 17 19816; gap of 100 bp 17 19816; gap of 100 bp 17 19816; gap of 100 bp 17 20557; contig of 741 bp in length 17 20557; contig of 741 bp in length 180 21379; contig of 722 bp in length 180 21379; contig of 722 bp in length 180 21379; contig of 724 bp in length 180 2223; gap of 180 bp 180 22303; contig of 720 bp in length 180 22303; contig of 720 bp in length 180 23013; contig of 720 bp in length
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f 730 bp in length
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f 724 bp in length
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f 717 bp in length
                                                      contig of 753 bp in length of
                                                                                                                                       10650: contig of 723 bp in length
10750: gap of 100 bp
11479: contig of 729 bp in length
                                                                                                                                                                                         11579; gap of 100 bp 12318; contig of 739 bp in length
                                                                                                                                                                                                                               12418: gap of 100 bp 13137: contig of 719 bp in length
                                                                                                                                                                                                                                                                  13237: gap of 100 bp
13959: contig of 722 bp in length
14059: gap of 100 bp
14785: contig of 505 bp in length
14885: gap of 100 bp
15580: contig of 695 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                             20: gap of 100 bp
17233: contig of 713 bp in length
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5158: contig of 723 bp in length
58: app of 100 bp
27960: contig of 702 bp in length
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708 bp
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26335: contig of 730 bp
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32090: contig of 744 bp
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25505: contig of
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23013: cont.
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35541 36261; cont
36262 36361; gap of
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37898: contig of 717 bp in length
98: gap of 100 bp
38730: contig of 732 bp in length
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37081: contig of 720 bp in length
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Silten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Ferestor, J., Ferreira, P., Fitzhugh, M., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Locke, K., Macdonald, P., Marquis, N., McEnn, P., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Santos, R., Severy, P., Stange-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC016982 230352 bp DNA HTG 26-FEB-2001
Mus musculus clone RP23-416H2, WORKING DRAFT SEQUENCE, 11 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 230352)
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                                                                                                                                                                                                                                                           ctttaactgggactggggcaaagtcaa-tcccacctttatacaatgaattgctgaagagg 2219
-----tgagatcatcagatggaggttcatcgggtttcaatgtcccgtatccttttgta 2040
                                                                                                              agaccttgaagttggcaacgcaggaaaacaggaactccaccctggtgccgtgaattgcag 2100
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------ Summary Statistics
Sequencing vector: M13; M77815; 39% of reads
Sequencing vector: Plasmid; n/a; 61% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Gaps

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Indels

Db 110701 TTTTCTCTTTTTTTGAGACAGTCTCAGTAACCCAGGCTGCTCTCAAGCTTGTGGCC 110642

28-FEB-1999

AF088189 23108 bp DNA ROD 28-F Mus musculus CD4 antigen (Cd4) gene, partial sequence. AF088189

DEFINITION

AF088189

ACCESSION

1305 ttettetetetgagacagagteteaetgtgtggeecaggetagteteaaaettgeggte 1364

71.8%; Pred. No. 0.002; ive 0; Mismatches 29;

Best Local Similarity 71.8 Matches 74; Conservative

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Insert size: 212000; agarose-fp Insert size: 212000; agarose-fp Insert size: 229352; sum-of-contigs Quality coverage: 9.5 in 020 bases; agarose-fp Quality coverage: 9.5 in 020 bases; agarose-fp (autity coverage: 9.5 in 020 bases; agarose-fp consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                           4200

6487 59418: contig of 52932 bp in length

59419 59518: gap of 100 bp

59519 69698: contig of 10180 bp in length

69699 69798: gap of 100 bp

69799 83694: contig of 13896 bp in length
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Consensus quality: 226546 bases at least Q40 Consensus quality: 228022 bases at least Q30 Consensus quality: 228658 bases at least Q20
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/clone_lib="RPCI-23 Female Mouse BAC"
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/note="assembly_fragment
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4260. .6386
/note="assembly_fragment"
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/note="assembly_fragment"
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158807. .191011
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/note="assembly_fragment"
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                                                                                                                 Hansen, R.K., McCready, P.M. and Sands, J.F.
Sequence Analysis of the 5' Flanking Region and First Intron of the
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Hansen, R.K., McCready, P.M. and Sands, J.F.
Hansen, R.K., McCready, P.M. and Sands, J.F.
Direct Submission
Submitted (31-A0G-1998) Biochemistry, Loma Linda, MT219, Loma
Linda, CA 92354, USA
Location/Qualifiers
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Pred. No. 0.0025;
0; Mismatches 70; Indels 0
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/gene="Cd4"
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/strain="B10.D2/nSnJ"
/db_xref="taxon:10090"
/chromosome="6"
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Matches 98; Conservative
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DB 64; Length 230352;

2.5%; Score 56.6;

Query Match

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Masahira Hattori, The Institute of Physical and Chemical Research
(EKIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,
Tsuruml-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mali:hattori@gsc.riken.go.jp, URL:http://hpp.gsc.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
On Oct 21, 2000 this sequence version replaced gi:8953895.
This work was done in collaboration with Dr. Hitchi Yatsuki, Dr.
Masayo Nishimura and Dr. Tsunehiro Mukai. (Saga Medical School,
Department of Biochemistry, Saga, 849-8501, Japan).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                       3086 ACTCTCTTTCCTGTAGTCTGAGCCTCCCAAGGACTGGGGGTTACAGGTGTGAGGGCACAAC 3145
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                                                                                                                                                                                                                     AP001917 68121 bp DNA ROD 21-OCT-2000 Mus musculus genomic DNA , chromosome 7, clone:B131T_{\odot}
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                                                                          1415 taggtagctcgcgttttaagctaagagctggaagatcctgatgtcctt 1462
                                                                                                   3146 AGCCAGTTTCTAGTTCTTAGCTGATATATCAAAACATTAAATGCACTT 3193
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Hattori, Watanabe, H., Toyoda, A. and Sakaki, Y. house mouse 68,121 genomic DNA
Published Only in DataBase (2000) In press
2 (bases 1 to 68121)
Hattori, M., Watanabe, H., Toyoda, A. and Sakaki, Y. Direct Submission
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17409 c 17842 g 16858
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05-DEC-2000

LOCUS AP001293 108333 bp DNA ROD 05-DEC-2000 DEFINITION Mus musculus genomic DNA, chromosome 7, clone:B131, complete

RESULT 10

AP001293

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Indicator, burnelist, roceintary, still cylindria, putinate; mus.

Hattori,M., Watanabe,H., Toyoda,A. and Sakaki,Y.

House mouse 108,333 genomic DNA

House mouse 108,333 genomic DNA

Lattori,M., Watanabe,H., Toyoda,A. and Sakaki,Y.

Experience of the colon of the c
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Mus musculus clone RP23-124B2, WORKING DRAFT SEQUENCE, 8 unordered
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-124B2
Unpublished
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 0.0027;
0; Mismatches 95; Indels 0;
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HTG; HTGS_PHASE1; HTGS_DRAFT
GI:11559491
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Best Local Similarity 54.3%;
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Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Choepel, T., Collander, B., Drown, A., Burkett, G., Castle, A., Choepel, T., Collangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Demino, M., Doyle, M., Fenestor, J., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McMeners, R., McMernan, R., Mornan, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Subramanian, V., Raymond, C., Riley, R., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Talamas, J., Tesfaye, S., Theodore, J., Zimmer, A. and Zody, M.

Submitted (10-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 10, 2001 this sequence version replaced gi:7139737.

All repeats were identified using Repeathasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
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Center clone name: 124_B_2

Center clone name: 124_B_2

Center clone name: 124_B_2

Sequencing vector: M3; M77815; 42% of reads
Sequencing vector: Plasmid; n/a; 58% of reads
Consensus quality: 210196 bases at least Q40
Consensus quality: 211074 bases at least Q30
Consensus quality: 211622 bases at least Q30
Insert size: 201000; agarose-fp
Insert size: 212361; sum-of-configs
Ouality coverage: 10.7 in Q20

* NOTE: This is a "working draft' sequence. It currently
consists of % contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17074 17173: gap of 100 bp
17174 23163: contig of 5990 bp in length
23164 23263: gap of 100 bp
23264 38610: contig of 15347 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14/2.73 of 100 pp
1375: gap of 100 pp
180586: contig of 33211 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0686: gap of 100 bp
213061: contig of 32375 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p of ' 100 bp contig of 19154 bp in length
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147275: contig of 58117 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17073: contig of 17073 bp in length
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/db_xref="taxon:10090"
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38711 57864: cont
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180587 180686:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
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/clone="RP23-124B2" /clone_lib="RPCI-23 Female Mouse BAC" 1. .17073

misc_feature

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carS gene; Cdknlc gene; cyclin-dependent kinase inhibitor lC; cysteinyl-tRNA-synthetase; IPL gene; Itm gene; Napl14 gene; nucleosome assembly protein 1-like 4 protein; Obph1 gene; oxysterol binding protein; Thrhl gene; Thrh2 gene; tumor necrosis factor receptor p60 homologue 1; tumor necrosis factor receptor p60 homologue 2; tumor suppressing subtransferable candidate 5.
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Submitted (17-MAR-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus domestious
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41769 CTCACTATGTAGGCCAGGGCAGTCTCTAGCTTAAGGTCCTCTTGCCTCAGCCTCCTAAAT 41710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41709 GCTGGGATTCCAGGTGTATATCCCGGCAGTCTCTGCAACTGTTCAAACTGGAAATCTTTA 41650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 281000)
Engemann,S., Strodicke,M., Paulsen,M., Franck,O., Reinhardt,R.,
Lane,N., Reik,W. and Walter,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   getgggetteceaggtgtgtgeeceacactaggtagetegegttttaagetaagagetgga 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1447 agatoctgatgtcotttaccatggtgggcatgttacaggttagttgactgaaaactagtt 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence and functional comparison in the beckwith-wiedemann region: implications for a novel imprinting centre and extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMU276505 281000 bp DNA ROD 26-JAN
Mus musculus genomic fragment, 281000 bp, chromosome 7.
AJ276505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 213061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       708 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 67;
Pred. No. 0.0028;
0; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                          vector_side:right"
51862 c 53839 g 53986 t
                                                                         /note="assembly_fragment"
89159. .147275
/note="assembly_fragment"
147376. .180586
                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
180687. .213061
/note="assembly_fragment
                   17174. .23163
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 41589 ATGTGGCTCAATAAAGCACCTAACCGGT 41562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1507 atctcgctgtgtaatgacctgcagtggt 1534
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vector_side:left"
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                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.5%;
Best Local Similarity 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 113; Conservative
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JOURNAL
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join(<31277. .31342,35572. .35662,37049. .37176,46179. .46291,
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/gene="Tnfrh1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .46291,
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47068. .47141.48531. .48627)
/gene="Tnfrh1"
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140377. .14057. | 141084,142468. .142590,
145511. .145624,146438. .146565,146958. .147085,
147169. .147274,147610. .147707,147985. .148174,
148724. .148724. .15226411. .152121,114073. .153154,
151189. .155255,157406. .157466,157904. .157988,
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/gene="Infrh1"
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/gene="Cars"
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13783. .13967
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16308. .16404
/gene="Obph1"
                                                                                                                                                    11978. .12149/gene="Obph1"
                                                                                                                                                                                                                                          12416. .12608
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14347. .14428
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/gene="Obph1"
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                                                                9688. .9772
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/gene="Obph1"
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            'gene="Obph1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number=10
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22181. .22
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22743. .22
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7906. .8110,9688. .9772,11978. .12149,12416. .12608,
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/db_xref="taxon:10092"
/db_xref="ta
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GROCEGOGSSPDASPSSLYCLPTSATIPDODLFPLACSALENDAFSIK SFRENAEDS
ARTODHSKATNESGSDLLDSPGGPWROTTYVEDVORELGELDETSOVPSTSKENSLM
WULKQLRFCMDLSSYVLPTFYLERSFLGKLSDYYYHGDLLSRAABEDDPYCRMKLY
LRWYLSGFYKKPKGIKKPYNPILGETFRCRWLHPQTNSHTFYIAEQVSHHPPVSAFYV
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DIAQYEQDGILHTLQRETMSGQTTFLGSPDSRHKRPSSDRRLRKASDQPSGHSQVTES
SGTPESCOPDLSDEDFVPGGESPCPRCRREVHRLKMLQEAVLSIQEAQQELHRHLSTM
LSSTYRAGQAPAPSLLQNPRSWFLLCIFLTCQLFINYILK"
3536. .3622
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TMTMELGGKVNIECEKNNLQAELDFKLKPFFGSSANINQISGKIMSGEEVLARLTGHW
DRDVFIKEESSGGTELFWTPSEEVRRQRLKRHTVLLEEQSELESERLWGHVTRAIREG
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                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Submitted Separation for Molekulare Genetik, Inhestrasse 73, 14195
Berlin, GREMAN
On Jan 27, 2001 this sequence version replaced gi:11191799.
related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
Location/Qualifiers
                                                                                                                  Direct Submission
Submitted (22-NOV-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
Revised by author 22-MAY-2000
3 (bases 1 to 281000)
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7265. .7345
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7478. .7578
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join(1432.
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7906. .811
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                                                                                            Engemann, S
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                              REMARK
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Summary Statistics 187635 bases at least 040
Consensus quality: 163578 bases at least 030
Consensus quality: 164611 bases at least 030
Consensus quality: 164611 bases at least 030
Consensus quality: 164611 bases at least 030
Estimated insert size: 165813; sum-of-contigs estimation
Betimated insert size: 165813; sum-of-contigs estimation
Quality coverage: 6.88 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
provided by the submittor.
* This sequence will be preserved.
* 1214: contig of 1214 bp in length
* 15700 15849: gap of unknown length
* 15700 15849: gap of unknown length
* 15850 31759: contig of 15439 bp in length
* 47299 47398: gap of unknown length
* 47299 47398: gap of unknown length
* 50192 50291: gap of unknown length
* 5150 52349: gap of unknown length
* 5150 52349: gap of unknown length
* 5150 53249: gap of unknown length
* 5150 5324
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39: contig of 11691 bp in length

19: gap of unknown length

1: contig of 1452 bp in length

1: gap of unknown length

1: gap of unknown length
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39178 a 43350 c 43117 g 39368 t 1500 others
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contig of 14713 bp in length
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58.0%; Pred. No. 0.0031;
iive 0; Mismatches 82;
                                                                                                                                    Center clone name: RPCI-23_413L18
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-413L18"
                            Web site: http://www.jgi.doe.gov
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                                                                                                           Center Project Name: 1895746
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                                                                              Project Information
                                                                                                                                                                                         Summary Statistics
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Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(<67525. .67596,72244. .72334,73711. .73838,76251. .76363,77140. .77213,77826. .77868,78677. .78828)
/gene="Tnfrh2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(67255. 67596,72244. .72334,73711. .73838,76251. .76363,77140. .77213,77826. .77868,78677. .78828)
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join(7256. .72334,73711. .73838,76251. .76363,77140. .77213,77826. .77857)
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37049. 37176
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Direct Submission

Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810404.

Center: Joint Genome Institute
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Mus musculus clone RP23-413L18, WORKING DRAFT SEQUENCE, 16 ordered
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 275809 CTCACTATGTAGGCCAGGCAGTCTTAGCTTAAGGTCCTCTTGCCTCAGCCTCCTAAAT 275868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 56; DB 94; Length 281000;
4.3%; Pred. No. 0.0028;
lve 0; Mismatches 95; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 275989 ATGTGGCTCAATAAAGCACCTAACCGGT 276016
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AC073787
AC073787.2 GI:9256796
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                48531. .48580
/gene="Tnfrhl"
/codon_start=1
                                                                                                                                                                                                                                                                                            /gene="Tnfrh1"
                                                                                                                                                                                                                                                                                                                                                  47068. .47141
/gene="Tnfrh1"
                                                                                                                                                                                                                                                                   .46291
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Matches 113; Conserv
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Gaps

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1 (bases 1 to 157996)
Montgomery,K.T., Grills,G., Han,J., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-DEC-1999) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 157996)
Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-JUL-2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
Bronx, NY. 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
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Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A. and Kucherlapati, R.
                         Submitted (14-JUL-2000) Department of Molecular Genetics, Albert
                                                                                    1405 tgcaccacactaggtagctcgcgttttaagctaagactggaagatcctgatgtccttta 1464
1345 ctagicicaaactigeggiceatitgicicacteateagaaigeigggeiteeaggigig 1404
                                                                                                                                                                                                                                                                                                                                     19026 157996 bp DNA ROD 14-JUL-2000 musculus chromosome 6 clone RP23-188E5 strain C57BL6/J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse High Throughput Sequencing Unpublished
                                                                                                                                                                                                         83158 AGTAGGGGTTGGTTGTTTGTTT 83184
                                                                                                                                                                               1465 ccatggtgggcatgttacaggttagtt 1491
                                                                                                                                                                                                                                                                                                                                                                                                         AC019026
AC019026.12 GI:8927595
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                                                                                                                                                                                                                                                                                                                                                                                    complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse,
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Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and cDNA sequences in Unigene. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Attempts are made to complete double stranded sequence for all regions. All sequence is completed to a standard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the annotation as Low Coverage. Low coverage Inhakages are verified by PCR product size verification or verification of forward and reverse reads from clones which span the low coverage area.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000 bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality.

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1008
                                          Dye-terminator Big Dye;
Phrap version 0.990319
                                                                                       Fraction of Phrap value < 40: 0.0011076
Error rate shown by Consed: 0.13 per 10,000 bases
                                                                                                                                                                                                                                                                                                                                                              35
                          puc18; LO8752
Dye-terminator
                                                                                                                                                  ----- Distribution of Quality < 40 Bases:
                                                                      157996
------Summary Statistics:
                                                                                                   Error rate shown by Consed:
Number of N's in consensus:
              Center project name:
                             Sequencing vector:
                                                           Assembly program:
                                                                       Contig length
                                                                                                                                                                                                                      7001
6000
7001
7001
1001
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                                        Chemistry:
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bases
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0.6																	
5 10 15 20 25 Phrap Value Range	Location/Qualifiers 1157996	/organism="Mus musculus"	/db_xrer="taxon:10090" /chromosome="6"	/clone="RP23-188E5"	448743 /rpt_family="(TG)n"	complement(21162138)	complement(21392274)	/rpt_family="B1_MM"	complement(22/52348) /rpt_family="ID3"	complement(33443682)	/rpt_ramily="L1_MM" 42514347	/rpt_family="CT-rich" 4348_4459	/rpt_family="(CATA)n"	46314754	/IPC_ramily="B4A" 48074841	/rpt_family="(CATA)n"	48634884
	FEATURES Source				repeat_region	repeat_region	repeat_region	1000	tepear_regrou	repeat_region	repeat_region	repeat region		repeat_region	repeat_region		repeat_region

ANNOTATION OF FEATURES: STSS are identified using ePCR (Genome Res. 7:541-550). Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features

http://sequence.aecom.yu.edu/cgibin/ws.exe/mouseDB/mouseSEQ/mouseseqtable.hts
Contact: jhan@sequence.aecom.yu.edu

Web site:

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 196858)

Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,

Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Carner, T.,

Addison, S., Paece, A., Williams, G., Bondih, D., Brooks, A., Brown, J.,

Buhay, C., Burkett, C., Chen, G., Chen, G., Chen, Z.,

Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,

Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gll, R.,

Gorrell, J. H., Gunarathe, P., Haller, G., Hernandez, J., Hogues, M.,

Rosar, C., Luu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,

Massey, E., McLeod, M.P., Mel, G., Moore, S., Morgan, M., Martin, R.,

Meal, D., Nelson, A., Newen, R., Nguyen, N., Oguh, M., Parish, B.,

Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, J., Watlington, S.,

Wullamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,

Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 32 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chases I to 196858)

Worley, K.C.

Direct Submission

Direct Submission

Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Feb 4, 2001 this sequence version replaced gi:12083996.

Center: Baylor College of Medicine
                                 Mus musculus chromosome 1 clone RP23-355F23, WORKING DRAFT SEQUENCE, 32 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                    AC084409.14 GI:12658711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard_name="11.MMHAP63FRD8.seq"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="B3"
9325. .9507
/rpt_family="LlMB1"
complement(10026. .10141)
/rpt_family="RLTRIIA"
10221. .10337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(14244...14333)
/rpt_family="B3"
complement(14343...14484)
/rpt_family="B1F"
15140...15306
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16277. 16296
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complement(16298. 16401)
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:complement 1
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16577. .16719
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                                                                                                                                                                                       complement(5749. .5813)
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complement(7176. .7345)
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8295 .8314 /rpt_family="Limbl"
8389 .8453
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8603 .9867
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5243. .5250
/note="Low coverage"
5338. .5670
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5089. 5164
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8101. .8244
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(5389, ,15503
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3308. .13328
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                                                                                                              misc_feature
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Gaps

; 0

40; Indels

Mismatches

0;

ilarity 66.4%; Conservative

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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                       30351: contig of 30351 bp in length 30451: gap of unknown length 49022: contig of 18471 bp in length 49022: gap of unknown length 63234: contig of 14212 bp in length 74342: contig of 11608 bp in length 75042: gap of unknown length
                                                                                                                                           gap of unknown length
contig of 13375 bp in length
gap of unknown length
contig of 8306 bp in length
                                                                                                                                                                                             gap of unknown length contig of 8146 bp in length
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of 7121 bp in length
                                                                                                                                                                                                                                            unknown length
of 7568 bp in length
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of 6524 bp in length
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of 6876 bp in length
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of 4850 bp in length
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of 3904 bp in length
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of 3755 bp in length
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of 2761 bp in length
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bp in length
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of 3099 bp in length
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unknown length
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of 4311 b
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                                                                                                                                                                                                                                                                                                                                                                                             unknown
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gap of unknown
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gap of unknown
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Location/Qualifiers

FEATURES source

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June 21, 2001, 13:27:01; Search time 8015.43 Seconds (without alignments) 4440.347 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX002124 Sequence	AF061804 Mus muscu	AF153058 Mus muscu	AC021220 Homo sapi	AC019251 Homo sapi	AC013745 Homo sapi	AC016982 Mus muscu	AF088189 Mus muscu
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DB	6	94	94	99	65	63	64	94
Query Match Length DB ID	100.0 12845	510	430	214348	135552	126330	230352	23108
Query	100.0	20.5	18.7	13.1	12.5	9.6	2.5	2.4
Score	2301	465	430	300.8	288.4	221.8	9.95	99
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                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-APR-1998) Molekulare Zellbiologie, Max Planck
Institut fuer physiologische und Klinische Forschung, Parkstrasse
1, Bad Nauheim 61231, Germany
Location/Qualifiers
                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                              Mus musculus fetal liver kinase 1 (Flk1) gene, intronic enhancer.
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                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kappel,A., Risau,W. and Breier,G. Prerequisite role of SCL/tal-1, GATA and Ets transcription factor binding sites for the in vivo function of Flk-1 gene regulatory
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                                                                                                                61 CTGGTACACAGCATGATAAAAGACAAATGGGACGGGGTCACAGTGGCTCCCGTCCCTTTCA 120
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                                                                                                                                                                                                                                                                                     Mus musculus tyrosine kinase FLK-1 minimal enhancer sequence.
AF153058
AF153058.1 GI:7963625
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94 c 112 g 116 t
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                                                                                                                                                             2257 aagtcaatcccacctttatacaatgaattgctgaagaggcctttt 2301
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Kappel,A., Risau,W. and Breier,G.
Direct Submission
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Matches 430; Conserv
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TITLE
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JOURNAL
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KEYWORDS
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Direct Submission
Submitted (15-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mno 63108, USA
On Nov 15, 2000 this sequence version replaced gi:9309528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 214348)
Waterston, R.H.
                                                     2138 aggaaaacaggaactccaccctggtgccgtgaattgcagagctgttgtgttgttgtg 2197
241 GGAGGTTCATCGGGTTTCAATGTCCCGTATCCTTTTGTAAGACCTTGAAGTTGGCAACGC 300
                                                                                                             301 AGGAAAACAGGAACTCCACCCTGGTGCCGTGAATTGCAGAGCTGTTGTGGTTTGTTGA 360
                                                                                                                                                                     HTG 15-NOV-2000 Sapiens chromosome 4 clone RP11-530117, WORKING DRAFT SEQUENCE, 38 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: plasmid; 13% of reads Chemistry: Dye-primer ET; 87% of reads Chemistry: Dye-primer ET; 87% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 195065 bases at least Q40 Consensus quality: 200600 bases at least Q20 Consensus quality: 203756 bases at least Q20 Insert size: 161000; agarose-fp Insert size: 210648; sum-of-contigs Quality coverage: 4.96 in Q20 bases; sum-of-contigs Quality coverage: 4.62 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
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1684: gap of unknown length
4194: contig of 2510 bp in length
424: gap of unknown length
6424: contig of 2130 bp in length
6524: gap of unknown length
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Waterston, R.H.
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13.1%; Score 300.8; DB 66; Length 214348;

Query Match

FEATURES SOURCE

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In Industrial Control of the Control
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                                                                                                                                                                                                Db 100808 AGTATATAATATGCATGTATGTGTGGAATTGGGGAATGTTTTCTCTTCCTCAGTTTCTC 100749
                                                                                                                                                                                                                                                                                                                                                     Db 100688 CCAGGGGAAGCGCACTAGA-AAATTGATAAAGGAAAATGAGACAAGGTCATAGATTCTCT 100630
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-5E20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 100570 ATCAGCAATTTAGTCAAATGTGTACATCCTATGTTCTATAAGAAATGTCAGTGGGTCCTT 100511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 100450 TGTAAGACCTTGAAGTTGGCAATGCAGGAAACAGGAACTCCACCCTAGCTCCATGAATT 100391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 100390 GCAGAACTGTTGTGTTGTTTTATGACCATCTGCCCATTCTTCCTGTTATGACACAGCTTG 100331
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Pred. No. 1e-63;
            78.28; Pie. 0;
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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                   Zimmer, A. and Zody, M.

Direct Submission
Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 5, 2000 this sequence version replaced gi:6649482.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                        ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L2005
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3392: con
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9526; cor
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527: gap or 32317: contig of 790 pr .2417: gap of 100 bp .33198: contig of 781 bp in length 33298: gap of 781 bp in length 34181: gap of 783 bp in length 34181: gap of 787 bp in length 9 35038: gap of 100 bp .2 35038: gap of 100 bp .35595: contig of 757 bp in length 96 35695: gap of 100 bp .35695: gap of 100 bp .36624: contig of 729 bp in length 96 36624: contig of 777 bp in length .477 
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41871: contig of //v ...
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49724: contig of 757 bp
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1853 agaagccactgcctcagcttctgcagctcagataccaaaggaagtctggtacacagcatg 1912
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                                                                                                                                                                                                                                                                                                                                                   Score 288.4; DB 65; Length 135552;
Pred. No. 1.2e-60;
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 101; Indels
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60186: contig of 776 bp in length
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61891: contig of 730 bp in length
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          7 50686: gap of 100 bp
7 51456: contig of 770 bp ir
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5 52434: gap of 100 bp
5 53204: contig of 770 bp ir
50586: contig of 762 bp
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54958:
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59310: con
         50686: gap of
51456: con
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Similarity 77.5%;
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AC013745/c LOCUS AC013745 126330 bp DNA HTG 13-JUL-2000 DEFINITION Homo sapiens chromosome 4 clone RP11-92P18 map 4, LOW-PASS SEQUENCE

us-09-445-201-1_copy_8260_10560.rge

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75 18974: gap of 100 bp

75 19716: contig of 742 bp in length

17 19816: gap of 100 bp

18 2057: contig of 741 bp in length

58 2057: gap of 100 bp

68 21479: gap of 100 bp

60 22193: contig of 741 bp in length
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E (Dases 1 to 126330)

Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collymore, A., Collymore, A., Cooke, P., Dearellano, K., Dearra, K., Collymore, A., Cooke, P., Dearellano, K., Demino, M., Donolan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardf, G., Hagos, B., Headrod, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Mardiffin, J., Medrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollarav, V., Rilagy, R., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Linct Submission

N. Submitted (15-Nov-1999) whitchead Institute/MIT center for Genome Research, 330 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6910837.

All repeats were identified using Repeatmasker:
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 126330)

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Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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100 bp
100 bp in length
100 bp
of 723 bp in length
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723 822: gap of 100 bp
823 1542: contig of 720 bp in length
1543 1642: gap of 100 bp
1643 2371: contig of 729 bp in length
2372 2471: gap of 100 bp
2472 33212: contig of 741 bp in length
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8161: con
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6622 7344: co
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AC013745.3 GI:9114527
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AUTHORS
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COMMENT

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AC016982.4 GI:13123354
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4.8%; Pred. No. 3.5e-44;
ve 0; Mismatches 135; Indels
31 38330: contig of 732 bp in length
31 38526: contig of 696 bp in length
27 39626: gap of 100 bp
27 40316: contig of 690 bp in length
4016: gap of 100 bp
17 44136: contig of 720 bp in length
37 4136: contig of 720 bp in length
37 4136: contig of 749 bp in length
86 42085: gap of 100 bp
86 42085: gap of 100 bp
86 42815: contig of 730 bp in length
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Shirten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Baltren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Golassa, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Ferestor, J., Ferrelra, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Forrest, C., Gage, D., Howland, J. C., Johnson, R., Jones, C., Landers, T., Lehocz, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Schjanovic, N., Santos, R., Severy, P., Stange-Thomann, N., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X.; Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC016982 230352 bp DNA HTG 26-FEB-2001
Mus musculus clone RP23-416H2, WORKING DRAFT SEQUENCE, 11 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                          88662 AGACCTTGAAGTTGGCAATGCAGGAAACAGGAACTCCACCCTAGCTCCATGAATTGCAG 88603
                                                                                                                                                                               2117 agaccttgaagttggcaacgcaggaaaacaggaactccaccctggtgccgtgaattgcag 2176
                                                                                                                                             2177 agctgttgtgttggtttgtgaccatctgcccattcttcctgttatgacagagcttgtgaa 2236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-416H2
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Center clone name: 416_H_2
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Insert size: 229352; sum-of-contigs
Quality coverage: 9.5 in Q20 bases; agarose-fp
Quality coverage: 8.8 in Q20 ba.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                              6487 59918: Contig of 52932 bp in length 59419 59518: gap of 100 bp 59519 69698: contig of 10180 bp in length 6699 69798: gap of 100 bp 69799 63694: contig of 13896 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83695 83794: gap of 100 bp
83795 101615: contig of 17821 bp in length
101616 101715: gap of 100 bp
11716 127243: contig of 25528 bp in length
127244 127343: gap of 100 bp
127344 158706: contig of 31363 bp in length
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/note="assembly_fragment"
6487. .59418
/note="assembly_fragment"
59519. .69698
/note="assembly_fragment"
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/note="assembly_fragment"
127344. 158706
/note="assembly_fragment"
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/note="assembly_fragment"
223085. .230352
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/note="assembly_fragment
clone_end:SP6
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/db_xref="taxon:10090"
/clone="RP23-416H2"
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                           2.5%; Score 56.6; DB 64; Length 230352; 71.8%; Pred. No. 0.0025; Live 0; Mismatches 29; Indels 0;
                                        Best Local Similarity 71.8
Matches 74; Conservative
                            Query Match
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Qy 1381 ttettetetetgagacagagteteactgtgtgggeecaggetagteteaaaettgeggte 1440

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1 (bases 1 to 23108)
Hansen, R.K., McCready, P.M. and Sands, J.F.
Sequence Analysis of the 5' Flanking Region and First Intron of the
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Db 110701 TITICCTCTTTTTTGAGACAGTCTCACTGTGTAACCCAGGCTGCTCTCAAGCTTGTGGCC 110642
                                                                                                                                                                                                                                                                                                                    Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hansen, R.K., McCready, P.M. and Sands, J.F.
Direct Submission
Submitted (31-AUG-1998) Biochemistry, Loma Linda, MT219, Loma Linda, CA 92354, USA
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17927. .18271
                                                                     1441 catttgtctcactcatcagaatgctgggcttccaggtgtgtgc 1483
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join(14561. .14699,23082. .>23108)
/gene="Cd4"
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58.3%; Pred. No. 0.0034;
Live 0; Mismatches 7
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/gene="Cd4"
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/organism="Mus musculus"
/strain="B10.D2/nSnJ"
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/chromosome="6"
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/gene="Cd4"
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/gene="Cd4"
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Masaahira Hattori, The Institute of Physical and Chemical Research

(RIKEM), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,

Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E.mail:hattoriegasc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

on oct 21, 2000 this sequence version replaced gi:8953895.

This work was done in collaboration with Dr. Hitomi Yatsuki, Dr.

Masayo Nishimura and Dr. Tsunehiro Mukai. (Saga Medical School,

Department of Blochemistry, Saga, Saga, 849-8501, Japan).
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                             AP001917 68121 bp DNA ROD 21-OCT-2000 MUS musculus genomic DNA , chromosome 7, clone:B131T. AP01917
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Mus musculus genomic DNA, chromosome 7, clone:B131, complete
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            Tackers 1 to 68121)

Hattori, M., Watanabe, H., Toyoda, A. and Sakaki, Y.
House Mouse 68, 121 genomic DNA
Published Only in DataBase (2000) In press
2 (bases 1 to 68121)

Hattori, M., Watanabe, H., Toyoda, A. and Sakaki, Y.
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17409 c 17842 g 16858 t
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/db_xref="taxon:10090"
/chromosome="7"
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Mus musculus clone RP23-124B2, WORKING DRAFT SEQUENCE, 8 unordered
                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-MAR-2000) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, The Institute of Physical and Chemical Research
(RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1
Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tells1-2-778-9923, Rax:81-42-778-9924)
This work was done in collaboration with Dr. Hitomi Yatsuki,
Dr. Masayo Nishimura and Dr. Tsunehiro Mukai. (Saga Medical School,
Department of Blochemistry, Saga, Saga, 849-8501, Japan).
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 10833)
Hattori, M., Watanabe, H., Toyoda, A. and Sakaki, Y. house mouse 108,333 genomic DNA
Published Only in DataBase (2000) In press
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54283 ACCACAATGAGATGTTTAAGAGGCCCAGAATATGAGAGTGTTAGAAACAGAACATTCGAA 54342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1463 gctgggcttccaggtgtgtgcaccaccactaggtagctcgcgttttaagctaagagctgga 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1523 agatoctgatgtcctttaccatggtgggcatgttacaggttagttgactgaaaactagtt 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match . 2.4%; Score 56; DB 94; Length 108333; Best Local Similarity 54.3%; Pred. No. 0.0034; Matches 113; Conservative 0; Mismatches 95; Indels 0;
                                                                                                                                                                                                                                                                        2 (bases 1 to 108333)
Hattori,M., Watanabe,H., Toyoda,A. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Mu:
1 (bases 1 to 21306).
1 (Pases 1 to 21306).
1 (Pases 1 to 11000, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-124B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="B131"
27103 c 27795 g 27790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .108333
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/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54343 ATGTGGCTCAATAAAGCACCTAACCGGT 54370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1583 atctcgctgtgtaatgacctgcagtggt 1610
Mus musculus DNA, clone:B131.
Mus musculus
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AC023248.3 GI:12061504
HTG; HTGS_PHASE1; HTGS_DRAFT.
house mouse.
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note="assembly_fragment"

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BASE COUNT
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Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
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Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Medlafim,J., Momeus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,P., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,M., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                           Submitted (10-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 10, 2001 this sequence version replaced gi:7139737.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M7815; 42% of reads
Sequencing vector: Plasmid; n/a; 58% of reads
Sequencing vector: Plasmid; n/a; 58% of reads
Chemistry: Dye-terminator: Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 211074 bases at least Q30
Consensus quality: 211074 bases at least Q30
Consensus quality: 211072 bases at least Q30
Insert size: 201000; agarcose-fp
Insert size: 212361; sum-of-contigs
Quality coverage: 11.3 in Q20
Quality coverage: 10.7 in Q20.

* NOTE: This is a 'working draft' sequence. It currently
consists of 8 contigs. The true order of the pleces
is in ot known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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17174 23163: contig of 5990 bp in length
23164 23263: gap of 100 bp
23264 38610: contig of 1537 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38511 38710: gap of 100 bp
38711 57864: contig of 19154 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57865 57964: gap of 100 bp 57965 89058: contig of 31094 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147276 147375: gap of 100 bp
147376 180586: contig of 33211 bp in length
180587 180686: gap of 100 bp
180687 213061: contig of 32375 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17073: contig of 17073 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oof 100 bp contig of 58117 bp in length
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/clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L5723
Center clone name: 124_B_2
Center clone name: Statistics
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector_side:left"
17174. .23163
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                                                                                                                                                                                                                                                                                                             Zimmer, A. and Zody, M. Direct Submission
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89159 14727
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JOURNAL
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cars gene; Cdknic gene; cyclin-dependent kinase inhibitor IC; cysteinyl-tRNA-synthetase; IPL gene; Itm gene; Napil4 gene; nucleosome assembly protein 1-like 4 protein; Obphi gene; oxysterol binding protein; Tirthl gene; Tinfry gene; tumor necrosis factor receptor p60 homologue 1; tumor necrosis factor receptor p60 homologue 2; tumor suppressing subtransferable candidate 5.
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Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
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Engemann,S., Strodicke,M., Paulsen,M., Franck,O., Reinhardt,R., Enac,M., Reik,W. and Walter,J.
Sequence and functional comparison in the beckwith-wiedemann region: implications for a novel imprinting centre and extended imprinting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41709 GCTGGGATTCCAGGTGTATATCCCGGCAGTCTCTGCAACTGTTCAAACTGGAAATCTTTA 41650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41769 CTCACTATGTAGGCCAGGGCAGTCTCTAGCTTAAGGTCCTCTTGCCTCAGCCTCCTAAAT 41710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41649 ACCACAATGAGATGTTTAAGAGGCCCAGAATATGAGAGTGTTAGAAACAGAACATTCGAA 41590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1523 agatectgatgteetttaeceatggtgggeatgttaeagggttagttgaetgaaaaettagtt 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1463 gctggggcttccagggtgtgtgcaccacactaggtagctcgcgttttaagctaagagctgga 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4%; Score 56; DB 67; Length 213061; 54.3%; Pred. No. 0.0035; Indels 0; Mismatches 95; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMU276505 281000 bp DNA ROD 26-JAN
Mus musculus genomic fragment, 281000 bp, chromosome 7.
AJ276505
                                                                                                                                                                                                                                                                                                                                                                                     708 others
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20519229
                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
52666 a 51862 c 53839 g 53986 t
/note="assembly_fragment"
                                                                                                                                                                                                                                                                    180687. .213061
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41589 ATGTGGCTCAATAAAGCACCTAACCGGT 41562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1583 atctcgctgtgtaatgacctgcagtggt 1610
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Revised by author 22-MAY-2000
3 (bases 1 to 281000)
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                                                                                                                                                                                                                                                                                                                               clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.48
Best Local Similarity 54.37
Matches 113; Conservative
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Engemann, S.
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     misc_feature
                                                        misc_feature
                                                                                                              misc_feature
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join(<31277. 31342,35572. 35662,37049. 37176,46179. 46291,47068. 47141,48531. 48627)
49noB="nnfth1"
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3564. 3564. 35662
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48531. .48580)
/gene="Tnfrh1"
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145511. 145624,146438. 146565,146958. 147085,
147169. 147274,147610. 147707,147985. 148174,
148724. 148792,152041. 152121,154073. 154154,
155199. 155255,157406. 157466,157904. 157988,
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30593. .130688
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/number=18

24.142. . 24268

/gene="Obph1"

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OGROCEGGSPDASPSSLYGLPTSATTPDODLFPLANSALENDAFSNKSERRAEDSD

AETODHSRKTNESGSDLLDSPGGPWRGTTVVEQVOBELGELDFSVQVETSERRAEDSD

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DRUKTTORKYVLEEGARGRAREHQUSLTPWRPQLFLLDPLTQEWRTYYFEDLSPWDPLK
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Direct Submission
Submitted (22-NOV-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
                                                                                                                                                    Engemann,S.

Direct Submission
Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(1432. 1455,3536. 3622,7265. 7345,7478. 7578,796,8110,9688. 9772,11978. 12149,12416. 12608,13793. 13967,14347. 14428,15828. 15926,16308. 16404,17790. 17898,21514. 21606,21996. 22086,22181. 22314,21942. 22028,22181. 22314,21956. 22086,25186. 22318,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791696. 27307,791
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On Jan 27, 2001 this sequence version replaced gi:11191799.
related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
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                                                                                           Berlin, GERMANY
TITLE
JOURNAL
                                                                                                                     REFERENCE
AUTHORS
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JOURNAL
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Center Project Name: 1895746
Center clone name: RPCI-23_413L18
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Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC073787 166513 bp DNA HTG 18-JUL-2000
Mus musculus clone RP23-413L18, WORKING DRAFT SEQUENCE, 16 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (abses 1 to 166513) DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 275809 CTCACTATGTAGGCCAGGGCAGTCTCTAGCTTAAGGTCCTCTTGCCTCAGCCTCCTAAAT 275868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 275929 ACCACAATGAGATGTTTAAGAGGCCCAGAATATGAGAGTGTTAGAAACAGAACATTCGAA 275988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1523 agatcctgatgtcctttaccatggtgggcatgttacaggttagttgactgaaaactagtt 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                               RPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 94; Length 281000;
Pred. No. 0.0035;
0; Mismatches 95; Indels 0;
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HTG; HTGS_PHASE2; HTGS_DRAFT
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DOE Joint Genome Institute.
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 54.3
Matches 113; Conservative
                                                                                                           /number=2
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                                                                                                                                                                                                                                                                                                           'number=5
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Best Local
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AUTHORS
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Web site: http://www.jgi.doe.gov

Project Information

Center: Joint Genome Institute Center Code: JGI

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Summary Statistics is Statistics in Statistics in Statistics in Statistics in Consensus quality: 163578 bases at least Q30 consensus quality: 164611 bases at least Q30 coulity coverage: 6.23 in Q20 bases; sum-of-contigs estimation Quality coverage: 6.23 in Q20 bases; sum-of-contigs estimation.

**NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. Gaps between the contigs estimation.

**NOTE: This is a 'working draft' sequence. It currently are represented as runs of N. The order of the pieces of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced to estimates that have provided by the submittor.

**This sequence will be preserved.

**This sequence as soon as it is available and the accession number will be preserved.

**This sequence will be prepared to the preserved.

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**This sequence as soon as it is available and the accession number will be preserved.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83043 CTGGCCTCCAACTAGTGATCCTCCTGCCTCAGCCTTCCAAATGCTGGGATTACAAATATG 83102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1361 tgcctgctattaattagttattcttctctctgagacagagtctcactgtgtgggcccagg 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of unknown length
contig of 11691 bp in length
gap of unknown length
contig of 1452 bp in length
gap of unknown length
contig of 20848 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI mouse BAC library 23"
43350 c 43117 g 39368 t 1500 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown length contig of 1701 bp in length gap of unknown length contig of 14713 bp in length.
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58.0%; Pred. No. 0.0039;
tive 0; Mismatches 82;
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/organism="Mus musculus"
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/clone="RP23-413L18"
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Matches 120; Conserv
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115609
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Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 15/99b)
Montgomery,K.T., Grills,G., Han,J., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A. and
Kucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-DEC-1999) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 157996)
Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R.,
Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A. and
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Montgomery,K.T., Grills,G., Han,J., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (06-JUL-2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 157996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submission Submitted (14-JUL-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave. Bronx, NY 10461, USA
                                  83103 TG-----CCTTAGCTGGCCCAAGGTATAAATCTACAGTGGGCAGTGGCTAATCTTTTGGA 83157
1481 tgcaccacactaggtagctcgcgttttaagctaagagctggaagatcctgatgtccttta 1540
                                                                                                                                                                                                                                                                            AC019026 157996 bp DNA ROD 14-JUL-2000 Mus musculus chromosome 6 clone RP23-188E5 strain C57BL6/J, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bronx, NY 10461, USA
On Jul 6, 2000 this sequence version replaced gi:7767645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse High Throughput Sequencing Unpublished
                                                                                                                                                  Db 83158 AGTAGGGGTTGGGTTGTTTGTTTGTT 83184
                                                                                                  1541 ccatggtgggcatgttacaggttagtt 1567
                                                                                                                                                                                                                                                                                                                                                                                  AC019026.12 GI:8927595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                            RESULT 14
AC019026
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                               a
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across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Attempts are made to complete double stranded sequence for all regions. All sequence is completed to a standard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the amnotation as Low Coverage. Low coverage linakages are verified by PCR product size verification or verification of forward and reverse reads from clones which span the low coverage area.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000 bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality.

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Dye-terminator Big Dye;
Phrap version 0.990319
157996
                                                                          Fraction of Phrap value < 40: 0.0011076
Error rate shown by Consed: 0.13 per 10,000 bases
                                                                                                                                                                                                                                                                                                                                35
                        pUC18; L08752
                                                                                                                                     ----- Distribution of Quality < 40 Bases:
                                                                                                                                                                                                                                                                                                                                30
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                                                                                                                                                                                                                                                                                                                                10 15 20 25
Phrap Value Range
------Summary Statistics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      448. 743
/rpt_family="(TG)n"
complement(2116. .2138)
/rpt_family="ID3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Bl_MM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="ID3"
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3344. .3682)
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="CT-rich"
4348. .4459
/rpt_family="(CATA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="AT_rich" 5089. .5164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1807. .4841
/rpt_family="(CATA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AT_rich" 5220. .5293
                                                                                                       Number of N's in consensus:
                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="6"
/clone="RP23-188E5"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'rpt_family="L1_MM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4631. .4754
/rpt_family="B4A"
4807. .4841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (2139
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          Center project name:
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                         Sequencing vector:
                                                   Assembly program:
                                                                  Contig length:
                                                                                                                                                                                                    7001
6001
7001
7001
7001
1001
                                   Chemistry:
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bases
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                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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STSS are identified using ePCR (Genome Res. 7:541-550).

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to EST and cDNA sequences in Unigene. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity

CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features

ANNOTATION OF FEATURES:

listing

http://sequence.aecom.yu.edu/cgi-bin/ws.exe/mouseDB/mouseSEQ/mouseseqtable.hts jhan@sequence.aecom.yu.edu

Contact:

AECOM

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standard_name="11.MMHAP63FRD8.seg"
3976. .13996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family "Ar_rich"

complement (14108 . 14212)

/rpt_family "B3"

14213 . 14243

/rpt_family "(RA)n"

/rpt_family "(RA)n"

/rpt_family "B3"

/rpt_family "B3"

/rpt_family "B3"

/rpt_family "B3"

15140 . 15306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MIR"
complement(16099. 16267)
/rpt_family="B3A"
16277. 16296
/rpt_family="(TTA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(10026. .10141)
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10221. .10337
                                                            /rpt_family="0RR1B"

complement(5749, .5813)

/rpt_family="B3A"

complement(7176, .7345)

/rpt_family="B2_Mm2"

/rpt_family="B2_Mm2"

/rpt_family="B2_Mm2"

/spt_family="B2_Mm2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(16298. .16401) /rpt_family="Lx9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(16402. .16519)
/rpt_family="B3A"
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8293. .8324
/rpt_family="LIMB1"
8389. .8453.
/rpt_family="LIMB1"
8454. .8601
                                                                                                                                                                                                                    8071. .8100
/rpt_family="(CAAA)n"
8101. .8244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="B1F"
complement(12335...1;
/rpt_family="B1_MM"...
13308...13328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="RSINE1"
15389, .15503
/rpt_family="(GA)n"
5243. .5250
/note="Low coverage"
                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Bl_MM"
8602. .8867
/rpt_family="L1MBl"
8923. .9077
                                                                                                                                                                                                  rpt_family="L1MB1"
                                                                                                                                                                                                                                                                  rpt_family="L1MB1"
245. .8292
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3737. .13888
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325. .9507
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16577. .167
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musses 1 to 196888]

Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Garner, T., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Davis, C., Liu, J., Hu, Gunaratho, P., Hallans, G., Morgan, R., Molly, S., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Massey, E., McLeod, M.P., McJ. G., Moore, S., Morgan, M., Martin, R., Massey, E., McLeod, M.P., McJ. G., Nowyen, N., Oguh, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Mulliamson, A., Mrensford, G., Zhou, X., Bouck, J., Hodgson, A., Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Worley, K. C.

Direct Submission

M. Dinett Submission

M. Dinett Submission

M. Dinett Submitted (01-Nov-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Paza, Houston, TX 77030, USA

On Feb 4, 2001 this sequence version replaced gi:12083996. Center project name: RP23-355P23

Center clone name: RP23-355P23

Center clone name: RP23-355P23

Center clone name: RP23-355P23

Center clone name: RP23-35SP23

Center clone name: RP23-35SP23

Chemistry: Dye-primer Bodipy: 72% of reads

Chemistry: Dye-terminator Big Dye: 27% of reads

Assembly program: Phrap; version 0,990329

Consensus quality: 1805059 bases at least 040

Consensus quality: 1802059 bases at least 020

Consensus quality: 180215 bases at least 020

Consensus quality: 180523; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; sum-of-contigs estimation

Quality coverage: 3.8x in 020 bases; sum-of-contigs estimation * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 32 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved. Db 129918 TCTCAAATTCAAAATCCTCCTGCCTCACTTTCCAAGTGATAGAACTACAGGTGTGTAC 129976 1425 totcaaaacttgcggtccatttgtctcactcatcagaatgctgggcttccaggtgtgtgc 1483 DNA HTG 17-FEB-2001 1 clone RP23-355F23, WORKING DRAFT Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu AC084409 196858 bp DNA Mus musculus chromosome 1 clon SEQUENCE, 32 unordered pieces. AC084409.14 GI:12658711 HTG; HTGS_PHASE1; HTGS_DRAFT. Center code: BCM Mus musculus house mouse. DEFINITION ORGANISM TITLE JOURNAL RESULT 1: AC084409 ACCESSION REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS VERSION KEYWORDS COMMENT SOURCE

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17: contig of 4161 bp in length
17: contig of 4161 bp in length
18: contig of 4242 bp in length
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19: gap of unknown length
19: gap of unknown length
19: contig of 3904 bp in length
19: contig of 3755 bp in length
19: gap of unknown length
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/clone="RP23-355F23" 55216 a 42662 c 41766 g 54102 t

BASE COUNT ORIGIN

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                           1; Gaps
 2.4%; Score 55; DB 77; Length 196858; 60.3%; Pred. No. 0.0061; ive 0; Mismatches 70; Indels 1;
                         Matches 108; Conservative
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Search completed: June 21, 2001, 18:10:18 Job time: 16997 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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This 12.8 kb DNA sequence spans the region from -6.65 kb relative to the transcriptional start site to +6.15 (located in the third exon) of the murine endothelial growth factor (VEGF) receptor-2 gene (Tk-1). This portion of the Filt-1 gene was isolated from the liver of mouse strain 129/SvJ by screening a phage library of liver flamming region of the gene, in combination with sequences within the 5'-flanking region of the gene, in combination with sequences located within the flirst intron, specifically and reproducibly target expression of heterologous DNA to angloblasts during early stages of vascular development and also to the vasculature of postnatal mice. The regulatory sequences of the first intron also function as an autonomous endothelium specific enhancer when fused to a sutonomous endothelium specific enhancer when fused to a sutonomous several potential binding sites for transcription factors of the Ets and GATA families. The invention provides a cnew claimed recombinant DNA (I) comprising at least one regulatory sequence from an intron of the Fik'l gene, or its homologue, to control expression in endothelial cells, in vivo, linked to (b) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA containing heterologous sequence controlled by endothelial cell specific regulator - from the Flk-1 gene, used to treat, prevent or diagnose vascular disease, tumours, also to screen
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these, or transformed cells, are used to identify agents (A), potential pharmaceuticals, that suppress, activate or enhance transcription of genes in endothelial cells. (I), vectors and (A) are used to direct or prevent (for antisense sequences) expression of genes specifically in endothelial cells, e.g. for treating angiogenesis, cancer, diabetic retinopathy, rheumatoid arthritis etc., and in wound healing, particularly for treating vascular cet., and in wound healing, proliferation of smooth muscle cells, specifically atherosclerosis), tumours and neuronal disorders. They may also be used to induce vascular disease in the transgenic animals or diagnostically, particularly for studying (mal)function, interactions and unregulated expression of endothelial products. (I) provide specific modulation of gene expression in endothelial cells, at all stages of development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cttttattgtatagtagcatatgtacctcttgcagtcagaatgagctgtctaaaggaacag 240
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                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                    Sequence 12845 BP; 3321 A; 2893 C; 2863 G; 3723 T; 45 other;
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2301;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0
Matches 2301; Conservative
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ctcaaacaaagtaagattccattattgaaaggcttgtttaagagcattttaactgcttgc ctatgttagggacagtgacttatttcatattgacaaatattatgccgattaattgaatat	ctatyltagygyacagtgacttatttcatattgacaaatattatgccgattaattgaata gactacccagttctatagctgtctcagggcagaccaagagcatctgtgatccagtcact 	taaatgccatttaaaatgcataatttgttggtctaggaataaac 	aatcacggcccaacacaagtctttaacaatgccaa 	catttaattaccaatgttttaaaaatatgtcattaattactaata 	caacacatgtacatcttattaagttgggtatattcagggtggcatagctgtagactattg 	cacatctgtgttggtgagccagtggagaactgcctcctggctgttctcagaaggccaca 	tgtcacggcattggctatttgccttggctctttgctaatactttattgacatggcct 	<pre>cttcgttcacgttcacttatttgcccaacaacgtcaatgccagctgaggccttaggagt </pre>	atctgttcttagtcagtgcgaattagaaagcctggatgcctgcc	ttcttcttcttctgagacagagtctcactgtgtggcccaggctagtctcaaacttgcggtc 	catttgtctcactcatcagaatgctgggcttccaggtgtgtgcaccacactaggtagctc 	gcgttttaagctaagagctggaagatcctgatgtcctttaccatggtgggcatgttacag 	gttagttgactgaaaactagttatctcgctgtgtaatgacctgcagtggtatgtat	caagat caagat	attggcctgagctcagagctttgattaatgagttgggaccccctagctattgctcattag 	acttacactatttttagttttgctctgagtttatgaatatgcatgtatgcatgaacttgg 	<pre>gagatattttcttccccaattccttttcctccatttaaatgtgctgtctttagaagcca </pre>
6 5	4 4 0	901	961	1021 9280	1081 9340	1141	1201	1261 9520	1321 9580	1381	1441	1501 9760	1561 9820	1621 9880	1681	1741	1801
oy oy	Oy do	Qy Db	Qy Dp	O.y	Qy Dp	Qy Dp	QY Db	Qy	Qy	O _Y	0y 0p	Qy Dp	Qy Dp	Oy Dp	Qy Db	OY Dp	Oy Dp

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Slit protein; frog; cell migration; neuronal; nerve axon; dendrite; leukocyte; graft rejection; HIV infection; antiinflammatory; wound repair; organ regeneration; asthma; arthritis; glomerulonephritis; cystic fibrosis; ulcerative colitis; Crohn's disease; multiple sclerosis; allergic encephalomyelitis; Alzheimmer's disease; coronary artery restenosis; ss.
                                  10479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New vertebrate DNA encoding a slit protein that is useful for treating graft rejection, inhibiting infection of a cell by human immunodeficiency virus, inhibiting inflammation, and for alding wound repair and organ regeneration.
2161 gtgccgtgaattgcagagctgttgtgttgttgttgtgaccatctgccatttttcttcctgtta
                                                                                                                                                                                                                                                               10540 gaattgctgaagaggcctttt 10560
                                                                                                                                                                                                                                                     2281 gaattgctgaagaggcctttt 2301
                                                                                                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                      Slit protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2000; 2000WO-US07040
                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-628199/60.
P-PSDB; B28151.
                                                                                                                                                                                                                                                                                                                 C63529 standard;
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Piwi family nucleic acids, polypeptides, and antibodies, useful in genetherapy of diseases such as cancer and in various research and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1374 ttagttattettetettetgagaeagagteteaetgtgtggeecaggetagteteaaaet 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a fragment of the genomic sequence containing the coding region for the mouse WRN gene (\rm X83004). The corresponding human gene (\rm X83001) encodes a protein related to Werner's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3656 TICTITITICTGTTAAGACAAAGTCTCACTAGGCCTAGGCTGACGGGGAACT 3597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding the WRN gene product \cdot useful for detection and treatment of Werner's syndrome, and related
                                                                                                                                                                          This sequence encodes the mouse piw1 family protein, designated miw1. The piw1 family nucleic acids and polypeptides are used in get therapy of diseases such as cancer and also in various research and diagnostic applications. The sequences can also be used to treat
                                                                                                                                                                                                                                                                  tissue dystrophy, anaemia, immunodeficiency, and male infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; WRN; Werner's syndrome; detection; diagnosis; autosomal; recessive disorder; phenotype; ss.
                                                                                                                                                                                                                                                                                                                                                                         2.0%; Score 46; DB 21; Length 4064;
63.6%; Pred. No. 0.013;
Live 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1434 tgcggtccatttgtctcactcatcagaatgctggggcttccaggtgtgtgc 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3596 TGGGGTTCCCCTGGCTTCACCTCCTGAGTCCTGAGATCACAGGCGTGTGC 3547
                                                                                                                                                                                                                                                                                                         Sequence 4064 BP; 1114 A; 978 C; 1077 G; 890 T; 5 other;
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                                                                                                                                 Claim 19; Page 180-185; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Partial mouse WRN genomic sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 7; 153pp; English.
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95US-0580539.
96US-0010835.
96US-0594242.
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.0%
Best Local Similarity 63.6%
Matches 70; Conservative
                                                                                          diagnostic applications -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-363671/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fu Y, Mulligan J,
    P-PSDB; Y90234.
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29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-1999
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                               The present sequence is the coding sequence for Xenopus slit protein. The slit protein is useful for altering or guiding cell migration of neural cells preferably nerve axons or dendrites, leukocytes or malignant cells expressing roundabout (robo) protein, by repulsion or inhibition. Also, the slit protein is useful for treating graft rejection, inhibiting the infection of a cell by HIV, inhibiting inflammation and in aiding wound repair and organ regeneration. In addition, the slit protein is useful for the treatment of conditions involving the migration of leukocytes, such as asthma, arthritis, glomerulonephritis, cystic fibrosis, ulcerative colitis, Crohn's disease, multiple sclerosis, allergic encephalomyelitis, Alzheimer's disease and coronary artery restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4114 CTGCAGAGTGATGTTGGCCTGAGCGCGGATCTTTGTCGAAGGAATTGGGATAAACGAGTC 4055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1729 attgctcattagacttacactatttttagttttgctctgagtttatgaatatgcatgtat 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piwi family protein; piwi; miwi; hiwi; gene therapy; tissue dystrophy; anaemia; immunodeficiency; male infertility; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3994 GCACTGGCACAGAAGATCATTCCCTTTCACAATGCATTGGGCTCCATTTTGACATTC 3938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcatgaacttgggaagatatttttttttcccccaattccttttcctccatttaaatgtgc 1845
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                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 5513;
                                                                                                                                                                                                                                                                                                       Sequence 5513 BP; 1668 A; 1216 C; 1211 G; 1418 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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/transl_except= (pos:450..452; aa:Xaa)
/transl_except= (pos:1337..1339; aa:Xaa)
/transl_except= (pos:5636..2638; aa:Xaa)
/note= "Xaa= Leu or Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_except= (pos:836.838; aa:Xaa)
/note= "Xaa= unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                      Score 55.4; DB 21;
Pred. No. 3.4e-05;
0; Mismatches 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse piwi gene, designated miwi.
Claim 1; Fig 1; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.4%;
Best Local Similarity 57.1%;
Matches 101; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0110901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repopulating haematopoietic progenitor cells (LTR-HPC), by comparing the expression of tissue transglutaminase (tTGase), a calcium dependent enzyme, in myeloid cells like blood or marrow to a standard. A higher level of tTGase expression compared to background expression, indicates the presence of LTR-HPC in the sample. Tissue TGase catalyses post-translational modification of proteins and is involved in apoptosis, cell adhesion, metastasis and extracellular matrix (ECM) assembly. It acts as a marker that distinguishes the LTR-HPC from other (im)mature
The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype, as well as related diseases.
                                                                                                                                                                                                          tattaattagttattcttctctctgagacagagtctcactgtgtggcccaggctagtct 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human tissue transglutaminase homologue-3"
/note= "GTP binding calcium dependent enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses a method of differentially identifying long-term
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Differentially identifying long-term repopulating hematopoietic progenitor cells using tissue transglutaminase, useful for improving medical procedures, including gene therapy
                                                                                                                                                                                                                                                                           caaacttgcggtccatttgtctcactcatcagaatgctgggcttccaggtgtgtgc 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tissue transglutaminase (tTGase) homologue-3 encoding mRNA.
                                                                                                                  2.0%; Score 45.6; DB 18; Length 51259; 62.1%; Pred. No. 0.067; ative 0; Mismatches 44; Indels 0;
                                                                    Sequence 51259 BP; 14533 A; 9635 C; 10266 G; 16825 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marker; allogeneic transplant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 48-50; 59pp; English.
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133..1182
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                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                         Z50462 standard; mRNA; 2362
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                                                                                                                                                     Conservative
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                                                                                                                                     Similarity
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                                                                                                                         Local Sim-
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                                                                                                                   Query Match
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Matches
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blood cells and is also useful for improved quantification of a mammal's haematopoietic competence. The method is useful for functional selection of progenitor cells, enabling allogeneis transplant procedures and ex vivo manipulation of HPC for use in gene therapy. The present sequence is an mRNA encoding a homologue of human tTGase, expressed in LTR-HPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences shown in V29330 to V29371 represent the 47 exons and flanking intronic sequences containing the complete coding region of the human calcium ion channel alpha 1 subunit gene and part of untranslated
                                                                                                                                                                                          1356 atgootgoctgotattaattagttattottottottotgagacagagtotoactgtgtggc 1415
                                                                                                                                                                                                                       1787 ATGCCTGCTAATTTTTATTTTTATTTTTTTTTTTGTAGACAAGGTCTCACTATATTGC 1728
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human nucleic acid associated with migraine and episodic ataxia type 2\, - useful for diagnosis and development of specific treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calcium ion channel alphal subunit exon 15/intron partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calcium ion channel alphal subunit; human; episodic ataxia type familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis;
                                                                                                                                                                 ;
0
                                                                                                                                   Score 45; DB 21; Length 2362; Pred. No. 0.019;
                                                                                                                                                                25; Indels
                                                                                      Sequence 2362 BP; 616 A; 593 C; 640 G; 513 T; 0 other;
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                                                                                                                                                                0; Mismatches
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/note= "partial sequence"
202..274
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/note= "partial sequence"
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                                                                                                                                   Query Match 2.0%;
Best Local Similarity 70.6%;
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                                                                                                                                                                 Conservative
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sequences. The channel is related to familial hemiplegic migraine (FHM) and/or episodic ataxia type 2 (EA-2) and is derived from, related to or associated with a gene present in humans on chromosome 19p13.1-13.2. The encoding gene can be used to localise or identify genes related to episodic neurological disorders, specifically migraine, FHM or EA-2, but also epilepsy. The isolated or a recombinant nucleic acid can also be used to distinguish between alleles of the corresponding gene. Cells and animals containing recombinant expression vectors comprising the nucleic acid can be useful in study, development and treatment of migraine, FHM, EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and natural or synthetic antibodies against the proteins can be used to
                                                                                                                                                                                                                                                                                                                                                                                    1363 cctgctattaattagttattcttctctgagacagagtctcactgtgtggcccaggct 1422
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                              Score 44; DB 19; Length 1110;
Pred. No. 0.024;
1; Mismatches 21; Indels
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rrcia PD, Garcia V, Giese K, Innis MA;

sam A, Kennedy GC, Kita D, Labat I;

ikowitz D, Pot D, Randazzo F, Reinhard C;

Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                           Sequence 1110 BP; 306 A; 287 C; 275 G; 239 T; 3 other;
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Jones WL, Kassam A, Kennedy GC, K
Lamson G, Leshkowitz D, Pot D, Ra
Stache-Crain B, Sudduth-Klinger J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216495 standard; cDNA; 810 BP
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Best Local Similarity 71.8%;
Matches 56; Conservative 1
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98US-0072910.
98US-0075954.
98US-0080114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
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The present invention describes a library of human polynucleotides comprising the sequences given in 21232 to 21779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in 212532 to 21779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct therapeutic purposes. The polynucleotides may also be used to construct concoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer, propertial procession in the concoded protein and management of colorectal cancer, breast cancer, and jung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
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Pred. No. 0.026;
0; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X02998 standard; DNA; 11901 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.9%; 64.3%; 1
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97US-0054646.
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Best Local Similarity 64.3:
Matches 81; Conservative
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                                                                                                                                                                                            X02956-X03048 and X22301-X22304 are overlapping BAC cenomic sequences containing alternatively spliced forms of human IL-Ira. Such fragments are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a member of the cytokine superfamily that is expected to inhibit inflammation by binding to the interleukin-1 receptor (IL-IR). It may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.
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Apo A1; low density lipoprotein; LDL; blood; therapy; atherosclerosis;
high density lipoprotein; HDL; cholesterol; coronary heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                       New isolated nucleic acid encoding the new human cytokine Tango-77 used to inhibit inflammation and to screen for specific modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.9%; Score 43.2; DB 20; Length 11901; 63.5%; Pred. No. 0.15;
tive 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11901 BP; 3552 A; 2724 C; 2438 G; 3179 T; 8 other;
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(YESH ) UNIV YESHIVA EINSTEIN COLLEGE
                                                                                                                                             Example 5; Figure 3; 226pp; English
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98US-0074497
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Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Apo Al genomic DNA.
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12-FEB-1998;
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This invention describes a novel method for the genetic treatment of hyperlipidemia by altering genes, in hepatocytes, for apoprotein (apo) B, E or Al. Low density lipoprotein (LDL) levels in the blood are reduced by altering an apo B gene (I) in a hepatocyte. The invention describes a method for the therapeutic and/or prophylactic method involving altering an apo E gene in hepatocytes by introducing the mutations Argl12Cys, Arg158Arg and a method for amellorating atherosclerosis by altering the apo Al gene in a hepatocyte so that the altered protein can dimerize. Altering expression of apo genes regulates levels of high and low density lipoprotein cholesterol. Altering expression of apo genes regulates levels of high and low density lipoprotein cholesterol. Altering expression of apo B, E and Algenes is used to treat or prevent atherosclerosis, coronary heart disease, Alzheinem's disease, hypobetalipoproteinemia, and dysbetalipoproteinemia. This sequence encodes the human Apo Al protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1386 ctcttctgagacagagtctcactgtgtggcccaggctagtctcaaacttgcggtccattt 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression augmenting sequence element; EASE; vector; recombinant protein; gene expression; Chinese hamster ovary; CHO;
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                                                                                                                                                                                                                                                                                                                                                                      Length 8966;
                                                                                                                                                                                                                                                                                                             Sequence 8966 BP; 2045 A; 2581 C; 2645 G; 1693 T; 2 other;
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0.18;
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                                                                                                                                                                                                                                                                                                                                                                    1.9%; Score 42.6;
58.1%; Pred. No. 0.
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/note= "EASE (Claim 1)"
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"EASE (Claim 1)"
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/note= "EASE (Claim 1)"
8671..14507
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"EASE (Claim 1)"
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8672..12273
Disclosure; Fig 3A-G; 106pp; English.
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1..14507
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                                                                                                                                                                                                                                                                                                                                                                                                        75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                    Expression augmenting sequence elements - used in vectors for expressing recombinant proteins at high levels in shorter periods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mammalian host cells. It was identified by cloning the integration site of a unique expression cassette encoding recombinant dimeric fundum necrosis factor receptor immunoglobulin Fc fusion protein from genomic DNA of a CHO 2A5-3 cell line expressing this protein at a high level. Expression vectors incorporating an BASE show a 2-to 8-fold improvement of recombinant protein expression levels in CHO host cells. The BASE sequence also facilitates high
                                                                                                                                                                                                                                                                                                                                                                                                                                         A 14507 bp DNA sequence (T73568) comprises a novel transcription regulatory element, expression augmenting sequence element (EASE), that facilitates high expression of recombinant proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EASE; expression augmenting sequence element; chinese hamster; ds.
                                                                       "the EASE sequence is preferably ligated
to DNA comprising nucleotides 14290-14507
(Claim 3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 42.2; DB 18; 59.9%; Pred. No. 0.31;
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              /*tag= g
/note= "EASE (Claim 1)"
14290..14507
/*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression in shorter periods of time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chinese hamster 2A5-3 lambda EASE DNA.
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10100..14923
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                                                                                                                                                                                                                                                          (IMMV) IMMUNEX CORP
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Matches 88; Conserv
 misc_feature
                                             misc_feature
                                                                                                                                   WO9725420-A1
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This invention describes a novel expression augmenting sequence element (EASE) (1) isolated from Chinese hanster cotary cells. (1) facilitates high expression of recombinant proteins in mammalian host cells in a short time period. (1) is used for improving expression of recombinant proteins 2-8 fold in stable cell pools when it is present in an expression vector. (1) improves recombinant protein expression in mammalian cells and facilitates the use of mammalian cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; prevention; treatment; protein therapy, gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma; sepsis; diabetes; AlDS; Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1424 greteaaaet-tgeggteeatttgteteaeteateagaatgetgggetteeaggtgtgtg 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1364 ctgctattaattagttattcttctctctgagacagagtctcactgtgtggcccaggcta 1423
                                                                                                                                                                                                                                                                    Improved expression of recombinant proteins in stable cell pools of mammalian cells comprises transforming cells with a vector containing an expression augmenting sequence element -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 14507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14507 BP; 4225 A; 2548 C; 3136 G; 4598 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis; psoriasis; digestive; endocrine; infection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein cDNA fragment containing gene 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 42.2; 59.9%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                       Claim 1; Column 17-30; 18pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant protein production.
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                                                                                               97US-0785150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88; Conservative
                                                                                                                                                                                                    Morris AE, Thomas JN,
                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
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Cricetulus sp
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                                                                                               13-JAN-1997;
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                               US6027915-A.
                                                               22-FEB-2000.
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09-MAR-2001 (first entry)
                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions of e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polypuclectides. Specific uses are absence of mutations in the new polypuclectides. Specific uses are described for each of the 70 polynuclectides. Based on which tissues the most highly expressed in, and include developing products for the diagnosts or treatment of cancer, tumours, neurodegenerative clasorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, asthma, osteoprosis, arthritis, psoriasis, dispestive/endocrine disorders, inflammation are represented in 197744 + 9707850 and the encoding nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                       Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 42; DB 20; Length 687; 69.5%; Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Indels
                                                                                                                                                                                                                                                                                     Feng P;
Lafleur DW;
Shi Y, Sopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 687 BP; 187 A; 148 C; 161 G; 187 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                  Duan R, Ebner R, Endress GA,
Florence KA, Komatsoulis GA,
Olsen HS, Rosen CA, Ruben SM,
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                                                                                        970S-0056369.
970S-0056369.
970S-005635.
970S-0056555.
970S-0056556.
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                                                                            98US-0092956
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970S-0056728.
                             98WO-US17044
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                                                                                                                                                                                                                                                                                  Brewer LA, I
Florence C,
Moore PA, Ol
Young PE;
                             18-AUG-1998;
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25-FEB-1999
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                                                                                           19-AUG-1
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C98178/c
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called human colon cancer antigens, given in B53234 to B54006. The human called human colon cancer antigens, given in B53234 to B54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; colon cancer antigens can have cytostatic, cardioactive, muscular; colon cancer immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders, reproductive disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. C98764 to C98772 and B54007 inceres.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
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                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection;
identification; cytostatic; cardioactive; neuroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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nephrotropic; antiinfective; antibacterial; gene therapy; wound;
neural disorder; immune system disorder; muscular disorder;
reproductive disorder; gastrointestinal disorder; renal disorder;
infectious disease; cardiovascular disorder; ss.
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Human colon cancer antigen nucleotide sequence SEQ ID NO:188.
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-hag 28; Indels
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Pred. No. 0.08
0; Mismatches
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ID V59610 standard; DNA; 1751 BP.
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Best Local Similarity
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This sequence represents a nucleic acid molecule designated Gene 101 from the human cDNA clone HLQAB52 (deposited as clone ATCC 97901 and ATCC 209047) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. V59502) for increasing the stability of the fused protein as compared to the human protein only:

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
   PERMETER SERVICE SERVI
                                                                             Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system, asthma; lymphocytic disease; brain; hepatic; lymphom; inflammation; ischaemic shock; Alzheimer's disease; restenosis; ALDS; cognitive disorder; schizophrenia; prostate; obsecolast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                  Human secreted protein gene 100 clone HLQAB52.
                                                                                                                                                                                                                                                                                                                                                                                  9705 - 0038621

9705 - 0038621

9705 - 0040161

9705 - 0040161

9705 - 00401331

9705 - 0040334

9705 - 0040331

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9705 - 0043313

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               06-JAN-1999 (first entry)
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07-MAR-1997
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11-APR-1997
11-APR-1997
11-APR-1997
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New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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9705-0047618.
9705-0047633.
9705-0047633.
9705-0048974.
9705-0048974.
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97US-0055724.
97US-0056630.
97US-0056631.
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970S-0056636.
970S-0056637.
970S-005664.
970S-0056845.
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97US-0056894
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P-PSDB; W74830.
23 - MAY - 1997;
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06 - JUN - 1997;
13 - JUN - 1997;
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16 - JUL - 1997;
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are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V59511 for described
                                                                                                    Gaps
                                                                                                                                                                                                                                   Human; purH; biallelic marker; single nucleotide polymorphism; SNP; diagnosis; prevention; treatment; prostate cancer; tumour; chromosome 1q34-q35; ds.
                                                                                        0;
                                                                        Score 41.8; DB 19; Length 1751;
Pred. No. 0.13;
0; Mismatches 42; Indels 0;
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                                                                                                                                       1690 GCGGACTGCAGTGGCGCAATCTCGGCTCACGCTCCCGCTTCCCGG 1642
                                                       Sequence 1751 BP; 405 A; 477 C; 476 G; 393 T; 0 other;
                                                                                                                                                                                                                       Human purH gene genomic DNA sequence.
                                                                                                                                                                                                                                                                            Location/Qualifiers
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/number= 5
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1 Similarity 61.5%;
67; Conservative (
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us-09-445-201-1_copy_8260_10560.rng

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

June 21, 2001, 13:30:07; Search time 150.46 Seconds

(without alignments)
2833.205 Million cell updates/sec

Title:
2301
Sequence:
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Scoring table:
Gapop 10.0, Gapext 1.0
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Total number of hits satisfying chosen parameters:

317530 seqs, 92630169 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: \cgn2_6/ptcdata/2/ina/FB_COMB.seq:*

6: \cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*

6: \cgn2_6/ptcdata/2/ina/PcTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

					SUMMARIES	
,		opp ,				
Result No.	Score	Query Match	Length	DB	ID	Description
	47.6	2.1	7218	-1	US-08-232-463-14	Sequence 14, Appl
7	45.6	2.0	51259	٣	US-08-781-891-209	209,
3	43.2	1.9	152331	4	US-09-128-155-16	16,
4	42.2	1.8	14507	m	US-08-785-150-1	,
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9 0	40.4	1.8	176373	4	US-09-128-155-17	17
c 2	40.2	1.7	380	-	US-08-126-587C-5	Š
အ ပ	40	1.7	1920	7	US-08-087-772A-1	1,
6	39.6	1.7	246240	7	US-08-724-394A-20	Sequence 20, Appl
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c 14	39.4	1.7	3912	4	US-09-115-954-1	Sequence 1, Appli
c 15	39.2	1.7	11725	~	US-08-756-506-1	1,
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	38.6	1.7	6949	~	US-08-488-011B-20	
c 24	38.6	1.7	6929	4	US-08-850-727-20	20,
c 25	38.6	1.7	6929	S	PCT-US95-10202-20	20,
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c 27	38.6	1.7	6919	2	PCT-US95-10220-20	Sequence 20, Appl

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US-08-699-628-1 US-08-454-557C-50 US-08-4340-4560-50 US-08-450-673C-50 PCT-US95-17111A-50 US-08-092-817-3 US-08-658-136-2 US-08-998-416-186 US-09-103-886-340-1 US-08-330-272-5 US-08-330-272-5 US-08-330-272-5 US-08-330-272-5 US-08-330-272-5 US-08-330-272-5 US-08-330-272-5 US-08-330-272-5 US-08-330-272-5	
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ALIGNMENTS

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RESULT 1

Sequence 14, Application US/08232463

Sequence 14, Application US/08232463

Sequence 14, Application US/08232463

Sequence 14, Application US/08232463

PERETI INFORMATION:
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STRATE: VA
COUNTRY: Alexandria
STRATE: VA
COUNTRY: USA
COMPTER READABLE FORM:
MEDIUM TYPE: FORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION NUMBER: BP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMA
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INFORMATION FOR SEQ ID NO: 209;

SEQUENCE CHARACTERISTICS

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     DB 1; Length 7218;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junna, Junna
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                    192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
2.1%; Score 47.6; DB :ilarity 8.7%; Pred. No. 0.0007; Conservative 208; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 209, Application US/08781891 Patent No. 6090620 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1623 agatgcttttttgcattt 1640
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Washington
                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
TITLE OF INVENTION: MOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER APPLICATION NUMBER: US 60/054,646
                                                                                                                                                                                                                                                                                                                                                                                                      Db 23803 CCACCCTGTTCCCCTTTTCCTCACCCTCCTGAGTGCTGGGATCACAGGCGTGTGC 23858
                                                                                                                                                                                                                                                                                                                                                                            1428 caaacttgcggtccattgtctcactcatcagaatgctgggcttccaggtgtgtgc 1483
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                                                                                                                                                                          Ouery Match 2.0%; Score 45.6; DB 3; Length 51259; Best Local Similarity 62.1%; Pred. No. 0.009; Matches 72; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Morris, Arvia E.
APPLICANT: Lee, Chi-chang
APPLICANT: Thomas, James N.
TITLE OF INVENTION: Expression Augmenting Sequence Elements
Patent No. 6027915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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1.9%; Score 43.2; DB 4
Best Local Similarity 63.5%; Pred. No. 0.091;
Matches 66; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09128155 Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08785150 Patent No. 6027915 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or
LENGTH: 51259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 16
LENGTH: 152331
                                                                             ; TOPOLOGY:
US-08-781-891-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-128-155-16
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EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

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1364 ctgctattaattagttattcttcttcttgagacagagtctcactgtgtggcccaggcta 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 CAGCCAAGATTTGTTTGTTTGTTTCCGAGAAAGGGTTTCTCTGTGTAGCCCTTGCTG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.8%; Score 42.2; DB 3; Length 14507;
Best Local Similarity 59.9%; Pred. No. 0.043;
Matches 88; Conservative 0; Mismatches 58; Indels 1;
                                                                                                                                                                                                                                                         OPERATING SYSTEM: Apple Operating System Software 7.1 SOFTWARE: Microsoft Word for Macintosh, Version 5.1a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
BARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1483 caccacactaggtagctcgcgttttaa 1509
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/586,509
FILING DATE: 11-JRN-96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 CIGACIACAGGCAAGCITGITITA 292
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/785,150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: 2A5-3 lambda CHO sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: No. 6027915 Relevant MOLECULE TYPE: DNA (genomic) ANTI-ERMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 14507 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chinese hamster
                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                  Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Chi
                                                                                                                                             USA
                                                                                                                                                                98101
                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                     STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-785-150-1
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                                                                                                                                                                                                                                      1378 ttattcttctctctgagacagagtctcactgtgtgggcccaggctagtctcaaacttgcg 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: 09404/05201
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER REPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-08-03
EARLIER FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 18
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy 1438 gtccatttgtctcactcatcagaatgctgggcttccaggtgtgtgcaccacact 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 40.4; DB 4; Length 176373;
59.6%; Pred. No. 0.68;
tive 0; Mismatches 46; Indels 0;
                                                                                                           Length 152331;
                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                              42; Indels
                                                                                                           Score 40.8; DB 4;
Pred. No. 0.47;
                                                                                                         Query Match
1.8%; Score 40.8; Di
Best Local Similarity 61.1%; Pred. No. 0.47
Matches 66; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08126587C Patent No. 5534438
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-128-155-17/c
; Sequence 17, Application US/09128155
; Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
COCATION: (1)...(152331)
COTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 68; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-126-587C-5/c
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RESULT
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              APPLICANT: Hayden, Michael
APPLICANT: Hayden, Michael
APPLICANT: Goldberg, Paul
APPLICANT: Andrew, Susan
APPLICANT: Rommens, Johanna M.
APPLICANT: Lin, Blaoyang
TITLE OF INVENTION: Process for Isolating Genes and the Gene
TITLE OF INVENTION: Causative of Huntington's Disease and Differential 3'
TITLE OF INVENTION: Polyadenylation in the Gene
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APPLICANT: Nabmias,
APPLICANT: Nabmias,
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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1.7%; Score 40.2; DB 1; Length 380;
Best Local Similarity 60.6%; Pred. No. 0.019;
Matches 66; Conservative 0; Mismatches 43; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1428 caaacttgoggtccatttgtctcactcatcagaatgctgggcttccagg 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 GCGGACTGCAGTGGCGCAATCTCGGCTCACTGAAAGCTCCGGCTTCCCGG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/126,587C
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson STREET: 1211 E. Morehead Street
CITY: Charlotte
STATE: No. 5534438th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08087772A Patent No. 5691155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: LAYCON Jr., Samuel G.
REGISTRATION NUMBER: 22,807
REFERENCE/DOCKET NUMBER: 3477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704-337-1561
TELEPHONE: 704-334-2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 704-334-2014
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHROMOSOME/SEGMENT: 4p16.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
POSITION IN GENOME:
GENERAL INFORMATION:
APPLICANT: Hayden
                                                                                                                                                                                                                                                                                                                                                                                      28234
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US-08-126-587C-5
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Gaps
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APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.7%; Score 40; DB 1; Length 1920; Best Local Similarity 63.5%; Pred. No. 0.058; Matches 61; Conservative 0; Mismatches 35; Indels
                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1442 atttgtctcactcatcagaatgctgggcttccaggt 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 TTCTGCCTCAACCTCCCAGTGCTGGGATTACAGAT 2
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
TYPE: nucleic acid
STRANDEDESS: single
                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
           FULL: POST C. CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3334
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
568..1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-087-772A-1
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STATE:
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1363 cctgctattaattagttattcttctctgagacagagtctcactgtgtgggcccaggct 1422
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1.7%; Score 39.6; DB 2; Length 246240;
Best Local Similarity 69.2%; Pred. No. 1.4;
Matches 54; Conservative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
CHARLY APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-QCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                     017957-000100
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/08724394A Patent No. 5872237
                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A 35,136
REFERENCE/DOCKET NUMBER: 01795
TELECOMMUICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION POR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
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Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Fitts, Renee A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Feder,
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US-08-724-394A-21
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APPLICANT:
APPLICANT:
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APPLICANT:
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69.2%; Pred. No. 1.4;
tive 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Trochihashi, Zenta
APPLICANT: TSuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724 2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
              REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246340 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      017957-000100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01795
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-576-0300
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                  TOPOLOGY: not relevant no of relevant necessary not relevant
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Db 95282 GGTCTCCAACTTCTGGGC 95299
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Best Local Similarity 69.2%
Matches 54; Conservative
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                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: not r
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                     APPLICANT: Rawlings, Christopher J
APPLICANT: Doe, Trudy R
TILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09115954B
; Patent No. 6200776
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.79
Best Local Similarity 71.29
Matches 52; Conservative
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        APPLICANT: Jupe, Steven C
                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-115-954-7
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; ORGANISM: Homo sapiens
US-09-115-954-1
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US-09-115-954-1/C
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US-08-756-506-1/c
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                                                                                                                                                                                                                                                                                                                  1363 cctgctattaattagttattcttctctgagacagagtctcactgtgtggcccaggct 1422
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69.2%; Pred. No. 1.4;
tive 0; Mismatches 24; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: BOTON, Walter F
APPLICANT: BOTON, Walter F
APPLICANT: Martin, Antoine M
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Jupe, Steven C
APPLICANT: Doe, Trudy R
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT FILING DATE: 1998-07-15
BARLIER APPLICATION NUMBER: EP97401714.7
SOFTWARE: PatentIN Ver. 2.0
                                                                                                    ; NAME/KEY: misc_feature
; LCATION: 1..246240
; OTHER INFEMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09115954B Patent No. 6200776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-115-954-7/c; Sequence 7, Application US/09115954B; Patent No. 6200776
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                           Db 95282 GGTCTCCAACTTCTGGGC 95299
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APPLICANT: Bril, Antoine M
APPLICANT: Khandoudi, Nassirah
APPLICANT: Martin, Xavier
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Best Local Similarity 69.24
Matches 54; Conservative
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TYPE: nucle STRANDEDNESS
                                                             MOLECULE TYPE:
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Best Local Similarity 71.2%; Pred. No. 0.13;
Matches 52; Conservative 0; Mismatches 21;
GENERAL INFORMATION:
APPLICANT: Boron, Walter F
APPLICANT: Bril, Antoine M
APPLICANT: Bril, Antoine M
APPLICANT: Khandoudi, Nassirah
APPLICANT: Wartin, Xavier
APPLICANT: Jupe, Steven C
APPLICANT: Doe, Trudy R
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT FILING DATE: 1998-07-15
EARLIER FILLNG DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
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Sequence 1, Application us/09755506

Patent No. 5905185

GENERAL INFORMATION:
APPLICANT: Cattingham. Ins R.
APPLICANT: Prometry Simon M.
APPLICANT: Prometry Simon M.
APPLICANT: Prometry Simon M.
APPLICANT: Specific Totaly A.
INTILE OF INVENTION: PROMESS:
TITLE OF INVENTION: ANIMALS
NUMBER OF SOURCES: A prometry of the second of
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM nucleic - nucleic search, using sw model
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em_esthum4:*
em_esthum5:*
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Maximum DB seq length: 200000000
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em_esthum1:*
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em_esthum7:*
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22. gb_est2:*
33. gb_est2:*
43. gb_est4:*
54. gb_est6:*
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Perfect score:
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em_estrolg: *
em_estro20: *
gb_est25: *
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117: gb_est48:*
118: gb_est48:*
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1120: gb_est50:*
120: gb_est50:*
121: gb_est51:*
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158: gb_est10:*
159: gb_est10:*
150: gb_est10
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9b_est110:* 9b_est111:* 9b_htc:* em_gss_hum:*	mgss_1 mgss_1 mgss_pss_1 mgss_pss_1 mgss_r mgs_r m _	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

ŏ	E4	ă O	
Description	A2364007 1M0110F03 A0126620 HS. 3032_B A0332669 HS. 3032_B A0332669 HS. 5004_A A2508851 1M0251G04 A2709930 RPC1-24-6 BE651040 UI_M-BH3- AW4551517 L0080A10- A2423401 1M0202C02 BF391061 UI_M-AO0- A166104973 UI_M-BG0- A1849973 UI_M-BG0- BF320748 UZ55h11.y A119334 MP80eb1.r AW826111 US21h04.x A2306979 1M0008H17 AV102206 AV102206 A2403474 1M0171B14 A2913824 RPCI-24-1 A26355903 CITBI-E1- A250622 AV096924 AQ355903 CITBI-E1- AZ410081 1M0182G10 BG07648 H31588F08- AZ410081 1M0182G10 BG07648 H31288F08- AZ71081 1M0182G10 BG07648 H31288F08- AZ711788 EST217740 AZ791331 2M0041010 AZ791331 1M048	AZ31825 1M0037H07 AAZ61578 mz87a12.r BE689422 uw54d12.y BF762191 1M0556123 BF121097 60177929 AZ46171 1M0267H18 AA004129 mg82403.r AZ431614 1M0165718 AZ333030 1M0155J19 AZ615574 1M0455D12 AZ100588 RPCI-23-2	sss 20-FEB-2001 ary Mus musculus genomic extebrata; Euteleostomi; ni; Muridae; Murinae; Mus. ", Duval,B., Hamil,C., ", F., Pedersen,T., Reilly A., von Niederhausern,A.
SUMMARIES	AZ815955 AZ364007 A AG32669 5 AZ3669930 8 AZ709930 8 AZ709930 6 AW490147 7 AW551517 A M8551517 A M8551517 A M8261049 A A119334 AA119334	AZ318225 AZ318225 AZ318225 BE689422 8 BE401678 9 AZ762191 4 BF711097 AA004129 3 AZ4431614 AA044824 3 AZ393030 6 AZ615574 8 AZ100588	ALIGNMENTS DNA plasmid UUGCLM libra R, DNA sequence. 873 Chordata; Craniata; Ve Rodentia; Sciurognathi Barber, M., Beacorn, T., Mahmoud, M., Meenen, Stokes, R., Tingey, R.,
Length DB	!	264 N 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	A2815965 746 bp 2M0084D06 R Mouse 10kb clone UUGC2M0084D06 R, A2815965.1 GI:1298587 GSS. Mus musculus Eukaryota; Metazoa; Ch Mammalia; Eutheria; Ro 1 (bases 1 to 746) Duni, D., Aoyagi, A., Ba Islam, H., Longacre, S., M., Rose, M., Rose, R., and Wright, D., Weiss, R.
% Query core Match	C	000000 0000000000000000000000000000000	AZ815965 2M0084D06R M clone UUGC2M AZ815965 AZ815965.1 (GSS. Mus musculus Eukaryota; M Mammalia; Eu 1 (bases 1 2 (base
Result No. Sc	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 AZ815965 LOCUS DEFINITION ACCESSION VERSION VERSION CETWORDS SOUNCE ONGANISM REFERENCE AUTHORS

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant valocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (q1|4732114|qplaF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into captured vector DNA, and transformed into captured vector DNA, and transformed into captured for amplicibil resistance."
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                    S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1083 acacatgtacatcttattaagttgggtatattcaggggtggcatagctgtagactattgca 1142
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Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bidg., 20 S. 2030 E., 84112, UsA
Tel: 801 585 506
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0084 row: D column: 06
Seq primer: CACACAGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 746.
Location/Qualifiers
L. 746
/organism="Mus musculus"
//clone="Teleff" | //cove="Mus" | //clone="Teleff" | //cove="Teleff" | //cove="Teleff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 TCGTTCACGTTCACTTATTTGCCCAACAACGTCAATGCCAGCTGAGGCCTTAGGAGAGATCAT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukarmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 586)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ364007 586 bp DNA GSS 02-OCT-2000 MDILOFO3F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0110F03 F, DNA sequence. AZ364007
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                                              tttgtctcactcatcagaatgctgggcttccaggtgtgtgcaccacactaggtagctcgc 1502
                                                                                                              1742 ottacactatttttagttttgctctgagtttatgaatatgcatgtatgcatgaacttggg 1801
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/db_xref="taxon:10090"
/clone="UGGIMO110F03"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: F column: 03
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Class: plasmid ends
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Fax: 801 585 7177
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AUTHORS
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COMMENT
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KEYWORDS
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/sex="Male"

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA
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HS_3032_B2_C02_MF CIT Approved Human Genomic Sperm Library D Homo
/lab_host="E: Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1474 aggigigigeaccacactaggiagetegegitttaagetaagagetggaagateetgatg 1533
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Matches 576; Conservative
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Best Local Similarity
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AQ126020/c
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1 (bases 1 to 404)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3032 Col=4 Row=F"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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AQ332669.2 GI:4341028
                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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sapiens genomic clone Plate=3032 Col=4 Row=F, DNA sequence
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                                                                                                                                                                                                                                                                                                                                  High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
T=1: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3032 row: F column: 4
Class: BAC ends
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                    AQ126020 GI:3503186
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Matches 135; Conservative
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99380589
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Aslam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                         University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 401 Queen Anne Avenue North, Seattle, WA 98109, USA 401 Queen Anne Avenue North, Seattle, WA 98109, USA 401 Queen Avenue North, Seattle, WA 98109, USA Enai: (206) 616-3618

Fax: (206) 616-3618

Enai: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu
Plate: 580 row: A column: 17
Seq primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; RPCI11 Human Male BAC Library"
75 c 93 g 113 t 5 others
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                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                          On Feb 19, 1999 this sequence version replaced gi:4130296.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
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3.4%; Score 78.6; DB 227; Length 464;
Best Local Similarity 66.5%; Pred. No. 1.2e-09;
Matches 125; Conservative 0; Mismatches 62; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=580 Col=17 Row=A"
/clone_lib="RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 464.
Location/Qualifiers
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(bases 1 to 464)
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AZ508851/c
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ORGANISM
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                                                                                                           AUTHORS
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KEYWORDS
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          SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114(pb]AR129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ/U9930 506 bp DNA GSS 24-JAN-2001
RPCI-24-67J15.TV RPCI-24 Mus musculus genomic clone RPCI-24-67J15,
DNA sequence.
                                                             Contact: Robert B. Weiss University of Utah Genome Center University of Utah University of Utah Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1411 giggcccaggctagictcaaactigcggiccattigictcactcatcagaaigcigggct 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1351 cctggatgcctgcctattaattagttattcttctctctgagacagagtctcactgt 1410
    Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58.2; DB 245; Length 556; Pred. No. 0.00027; 0; Mismatches 43; Indels 0;
                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Insert Length: 10000 Std Error: 0.00
Plate: 0351 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                 1. .556
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                         High quality sequence stop: 556.
                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0351G04"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex-"Male"
                     plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.1
Matches 84; Conservative
                                                                                                     Unive.
Rm. 308, Bic
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                                        JOURNAL
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TITLE
                                                           COMMENT
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SM Mus musculus

Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 506)

S Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell.D., de Jong,P. and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-24

Mu Dupublished (1999)

Cother_GSSs: RPCI-24-67J1S.TJ

Cottact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

The Institute for Genomic Research

The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdcjong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male" //cell_type="Spleen/Brain" //cell_type="Spleen/Brain" //cell_type="YaraBaCl; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBACl cloning vector at the BamH1 sites using Mbol partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE651040 256 bp mRNA EST 06-SEP-2000 UI-M-BH3-asy-e-09-0-UI.r1 NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-asy-e-09-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1334 cagigogaattagaaagociggatgocigccigciattaattagiattctictictic 1393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5%; Score 56.6; DB 248; Length 506; 60.9%; Pred. No. 0.00069; Live 0; Mismatches 69; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-67J15"
/clone_lib="RPCI-24"
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1..506
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BE651040.1 GI:9976864
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Best Local Similarity 60.9
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends.
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RESULT

LOCUS

SOURCE

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/clone="Ul-daxon:10090"
/clone="Ul-daxon:10090"
/clone="Ul-"NIH_BMAP_M_S4"
/dev_stage="27-32 dayg"
/dab_host="DH010B (Life Technologies)"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
polylihker; Site_1: Not 1; Site_2: ECO R1; The
NIH_BMAP_M_S4 libraries from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bubbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hipocoampus) after a series of subtractions to reduce the
representation of CDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S3.'
NIH_BMAP_M_S3.' NIH_BMAP_M_S3.', NIH_BMAP_M_S3.'
NIH_BMAP_M_S3.' NIH_BMAP_M_S3.' NIH_BMAP_M_S3.'
NIH_BMAP_M_S3.' NIH_BMAP_M_S3.' And NIH_BMAP_M_S3.'
NIH_BMAP_M_S3.' I clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.' NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.'
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles (subtracted the
NIH_BMAP_M_S3.' Ilbrary. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                     Email: mEST@mail.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP CDNAs whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 52-169, >PBIDIO#SINE/Alu
                              Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two\ approaches\ to\ facilitate\ gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1365 tgctattaattagttattcttctcttctgagacagagtctcactgtgtggcccaggctag 1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                       Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 t
                                                                                                                                                                                          Contact: Chin, H
National Institute of Mental Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                             Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13 Reverse
(bases 1 to 256)
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                                                                                                                                                                                                                                                                                                                       Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                20892-9643, USA
                                                                                              discovery
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ORIGIN
                                                                                                                          JOURNAL
MEDLINE
REFERENCE
                           AUTHORS
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June 1 were transfer of track that was present in the sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dT track served to identify it as a clone from the normalized brain stems library CDNA library Preparation: M B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNA whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Quantifiers

1. 257

/organism="Mus musculus"
/strain="CSTBL/60"
/db_xafe="taxon:10090"
/clone="UI-W-BH3-asy-e-08-0-UI"
/clone="UI-W-BH3-asy-e-08-0-UI"
/clone="UI-W-BH3-asy-e-08-0-UI"
/clone="UI-W-BH3-asy-e-08-0-UI"
/clone="UI-W-BH3-asy-e-08-0-UI"
/clone="UI-W-BH3-asy-e-08-0-UI"
/clone="UI-W-BH3-BMAP_M-S4"
/dev_stage="127-32 days"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
normalized library is a subtracted library of a series
/ultimately derived from a mixture of individually tagged
normalized library is a subtracted library of series of subtractions of reduce the representation of coMNs from which ESTS had already been generated. The following serially subtracted libraries
// NIH_BMAP_M-S3.3, NIH_BMAP_M-S3.1, NIH_BMAP_M-S3.1, NIH_BMAP_M-S3.1, NIH_BMAP_M-S3.2, and NIH_BMAP_M-S3.1, NIH_BMAP_M-S3.2, and NIH_BMAP_M-S3.2, and NIH_BMAP_M-S3.3, NIH_BMAP_M-S3.3, and nihamap_M-S3.3, NIH_BMAP_M-S3.3, and nihamap_M-S3.3, NIH_BMAP_M-S3.3, and nihamap_M-S3.3, NIH_BMAP_M-S3.3, nihamap_M-S3.3, nihamap_M-S3
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Normalization and subtraction: two approaches to facilitate gene
                           AW490147 257 bp mRNA EST 24-FEB-2000 UI-M-BH3-asy-e-08-0-UI.sl NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-asy-e-08-0-UI 3', mRNA sequence.
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National Institute of Mental Health
Notional Institute of Nornal Health
20802-9643, USA
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                                                                                                                                                                        AW490147
AW490147.1 GI:7060417
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Fax: 301 443 9890
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Site_1: SalI; Site_2: NotI; Total RNAs were extracted from
Site_1of salI; Site_2: NotI; Total RNAs was synthesized
by Gibco's kit with an Oligo(dT) primer [NotI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka,T.S., Jarada,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J. Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. Illi, Becker,K.G. and Ko,M.S.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
/dLxref="taxon:10090"
/clone="L0080A10"
/clone="L0080A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW551517 652 bp mRNA EST 31-AUG-2000
L0080AlO-3 Mouse El2.5 Female Mesonephros and Gonads cDNA Library
Mus musculus cDNA clone L0080AlO 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 652)
described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996). TAG_LIB=NIH_BMAP_M_S4
TAG_LISUE-brain-stems
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                                                                                                                                                                                                                                                                                                     209 IGTEGTTGTTTTTTTTTTTTTTTCTCTGACACAGTATCACTATGTAGCCCAGACTGT 150
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
Asia Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plater: LOONS row: A column: 10
Seq primer: -21M3 Forward
High quality sequence stop: 652
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                                                                                                                                                                                            DB 116; Length 257;
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                                                                                                                                                                                            Score 55;
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/lab_host="DH10B"
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                                                                                                                                                                                                                                    Conservative
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'-haa 79; Conserva
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RESULT

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by long-range high fidelity PCR using Takara's Ex map polymerase. Then, the cDNAs were purified by phenol/Chloroform and by Centricon 100. The cDNAs were digested with SalI and NotI enzymes. Then, the CDNAs were size selected by Gibco's Size Fractionation Column. The CDNAs were cloned into Sall/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
  Then, cDNAs were amplified
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 559)
Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., Museuchi,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ423401 559 bp DNA GSS 03-OCT-2000 1M0202C02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0202C02 R, DNA sequence.
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                       2.4%; Score 55; DB 117; Length 652; 60.3%; Pred. No. 0.0019;
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free linkers by Centricon 100.
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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High quality sequence stop: 559.
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/clone="UUGC1M0202C02"
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Fax: 801 585 7177
Email: ddunn@genet
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwNAC (gilfy13114 gplAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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The sequence contained an oligo-dT track that was present in the
                            musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9250
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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Pred. No. 0.0021;
0; Mismatches 62; Indels 0;
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                                                    Laboratory Mouse DNA Resource
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BF391061
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KEYWORDS
SOURCE
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/strain="Sprague-Dawley"
/strain="Sprague-Dawley"
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/clone_lib="UI.R-CAl.bcf-f-12-0-UI"
/clone_lib="Wetor: pT73D-Pac (Pharmacia) with a modified
/note="weetor: pT73D-Pac (Pharmacia) with a modified
/note in Site al. Not I; Site 2: Eco RI; The UI-R-CAl
/nibrary is a subtracted library described in (Bonaldo, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
/previously described in (Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized pineal glands library cDNA Library Preparation: M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 320)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 16-133, >PB1D10#SINE/Alu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI838610 320 bp mRNA EST 14-JUL-1999 UI-M-AOO-abz-f-12-0-UI.sl NIH_BMAP_MPG Mus musculus cDNA clone UI-M-AOO-abz-f-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 TTTTTTTTTTTTTGCTTGTTTTATGAGACAGGCATCACTATATACCCCAGGCTAGCCT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1428 caaacttgcggtccatttgtctcactcatcagaatgctgggcttccaggtgtgtgc 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 GGAACTTGCTATCCTACTGTTCCAACCTCCAGAGTGCTGGAAGGTGTATTC 120
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53.6; DB 148; Length 432; Pred. No. 0.004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                 /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                           Location/Qualifiers
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                                                     Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ=GAACCG
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AI838610.1 GI:5472823
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Best Local Similarity 60...
Best Local 77; Conservative
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301 443 9890
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                                                                                  POLYA-Yes.
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AI838610
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TITLE
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                                                                                                           FEATURES
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/strain="C57BL/6"
/db.xref="taxon:10090"
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/clone="UI-W-A00-abz-f-12-0-UI"
/clone="UI-N-W-MPG"
/dev_stage="27-32 days"
/dev_stag
Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP CDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 1-44, >AT_rich#Low_complexity 103-204, >PBID10#SINE/Alu POLYA-YES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1385 tetettetgagacagagteteaetgtgtggeecaggetagteteaaaettgeggteeatt 1444
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fat: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Score 53.4; DB 102; Length 320;
69.9%; Pred. No. 0.0042;
Live 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                           1. .320
/organism="Mus musculus"
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed and normalized by Bento Soares and M.Patima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 431)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
              This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new data is from the 3' end similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized spinal cord library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3%; Score 53.4; DB 23; Length 4 69.9%; Pred. No. 0.0045;
Live 0; Mismatches 31; Indels
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                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE;719561"
/clone_lib="Soares mouse NML"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Rès. 6 (9), 791-806 (1996)
97044477
                                                                                                                                       High quality sequence stop: 321.
Location/Qualifiers
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/clone_ib="10" about all by the control of c
available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP CDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 1-41. >AT_rich#Low_complexity 100-201, >PBID10#SINE/Alu POLYA*FS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NII-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1385 tetettetgagacagagteteaetgtgtgggeecaggetagteteaaaettgeggteeatt 1444
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Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffreg Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/organism="Mus musculus"
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TAG_TISSUE=spinal-cord
TAG_SEQ=TCGAA"
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Location/Qualifiers
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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	PCT-US95-10203-20
Seduence 70.	PCT-US95-10220-20

Sequence 1, Appll Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 1, Appl Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli		
C 28 38.4 1.7 501 3 US-08-699-628-1 29 38.4 1.7 2520 2 US-08-454-557C-50 31 38.4 1.7 2520 2 US-08-450-50-50 32 38.4 1.7 2520 2 US-08-450-50-50 33 38.2 1.7 2520 5 PCT-US95-17111A-50 C 33 38.2 1.7 2520 5 PCT-US95-17111A-50 C 35 38 1.7 40352 3 US-08-846-111D-15 36 38 1.7 40352 3 US-08-658-136-2 37 38 1.7 53526 3 US-08-658-136-2 38 37.4 1.6 7720 4 US-08-998-416-186 37 1.6 4084 3 US-08-698-416-186 41 37 1.6 4460 4 US-09-103-875-4 42 36.8 1.6 4922 2 US-08-330-22-5 43 36.8 1.6 4922 5 US-08-330-22-5 44 36.6 1.6 5375 3 US-08-55-123-7 C 45 36.6 1.6 10825 3 US-08-55-123-7	ALIGNMENTS	RESULT 1 US-08-232-463-14 Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 APPLICANT: BCHKNER, F. APPLICANT: SCHETELINGER, F. APPLICANT: FALKENER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS SCHORES: 52 CORRESPONDENCE ADDRES: 53 CORPUTER: READABLE FORM: MEDIUM TYPE: LEMP PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OMPUTER: IBM PC compatible OMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OMPUTER: SYSTEM: RELEASE #1.0, Version #1.25 FILING DATE: US/08/23,463 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT. SLEPPIN REGISTRATION NUMBER: 29,768 REFERENCE/POCKET NUMBER: 30472/114 IMMU TELEPHONE: CACHORITY INFORMATION: NAME: BENT. (703)836-9300 TELEX: 899149 INFORMATION POR SED ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH : 7218 base pairs TYPE: nucleic acid STRANDEDNESS: Single INMEDIATE SOURCE: CLONE: PTSQUENCE CLONE: PTSQUENCE CLONE: PTSQUENCE CLONE: PTSQUENCE CLONE: PTSQUENCE

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                                                                 1127 tcacggcattggctatttgccttggctctttgctaatactttattgacatggcctcatct 1186
                                                                                      1187 tcgttcacgttcacttatttgcccaacaacgtcaatgccagctgaggccttaggagtcat 1246
                                                                                                                                                      1307 cttctcttctgagacagagtctcactgtgtggcccaggctagtctcaaacttgcggtcca 1366
                                                                                                                                                                                                                                                                                                                                                    tttgtctcactcatcagaatgctggggcttccaggtgtgtgcaccacactaggtagctcgc 1426
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     Length 7218;
Query Match 2.1%; Score 47.6; DB 1; Length 7 Best Local Similarity 8.7%; Pred. No. 0.00074; Matches 38; Conservative 208; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 209, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Schillenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
UNMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAFING SYSTEM: PC-DOS/MS-DOS
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N: 800
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(206) 682-6031
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FILING DATE: 27-DEC
CLASSIFICATION: 800
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STATE: Washing
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US-08-781-891-209
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APPLICANT: Pan, Yang
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PELLING DATE: 1998-08-03
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                    Db 23803 CCACCCCGTTTTCCTCACCCTCTGAGTGCTGGGATCACAGGCGTGTGC 23858
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Pred. No. 0.095;
0; Mismatches 38; Indels 0;
                                                                                                                                                                         Score 45.6; DB 3; Length 51259;
Pred. No. 0.0095;
0; Mismatches 44; Indels 0;
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APPLICANT: Morris, Arvia E.
APPLICANT: Lee, Chi-Chang
APPLICANT: Thomas, James N.
TITLE OF INVENTION: Expression Augmenting Sequence Elements
Patent No. 6027915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09128155
Patent No. 6117654
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; LOCATION: (1)...(152331)
; CTHER INFORMATION: n = A,T,C or
US-09-128-155-16
INFORMATION FOR SEQ ID NO: 209:
                                                                                                                                                                     Query Match 2.0%;
Best Local Similarity 62.1%;
Matches 72; Conservative
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Best Local Similarity 63.5%;
Matches 66; Conservative (
                SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 16
LENGTH: 152331
                                                                                            ; TOPOLOGY:
US-08-781-891-209
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US-09-128-155-16
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US-08-785-150-1
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EARLIER APPLICATION NUMBER: US 60/054,646 EARLIER FILING DATE: 1997-08-04 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PASLSEQ for Windows Version 3.0
                                                                                                    SEQ ID NO 16
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                                                                                                                                                                                                 FEATURE:
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APPLICANT: Pan, Yang
TITLE OF INVERTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.9%; Score 42.2; DB 3; Length 14507;
Best Local Similarity 59.9%; Pred. No. 0.046;
Matches 88; Conservative 0; Mismatches 58; Indels 1;
                                                                                                                                                                                                                                                          OPERATING SYSTEM: Apple Operating System Software 7.1 SOFTWARE: Microsoft Word for Macintosh, Version 5.1a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: Ú$/08/586,509
FILING DATE: 11-JAN-96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/785,150
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CLONE: 2A5-3 lambda CHO sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,693
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2841
TELECOMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR ESQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14507 base pairs
TYPE: nucleic acid
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09128155 Patent No. 6117654
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No. 6027915 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                    Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chin
                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                  98101
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                                                                                                                                               COUNTRY:
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1999-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASUSEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                      Query Match 1.8%; Score 40.8; DB 4; Length 152331; Best Local Similarity 61.1%; Pred. No. 0.49; Matches 66; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 40.4; DB 4; Length 176373; 59.6%; Pred. No. 0.71; tive 0; Mismatches 46; Indels 0;
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; Patent No. 5534438
                                                                                     ; NAME/KEY: misc_feature; LOCATION: (1)...(15231); OTHER INFORMATION: n = A,T,C or G US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTION: (1)...(176373); OTHER INFORMATION: n = A,T,C or GUS-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Conservative
                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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US-08-126-587C-5/c
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LENGTH: 152331
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GENERAL INFORMATION:
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; LOCATION:
US-08-087-772A-1
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                                                       APPLICANT: Addrew, Susan
APPLICANT: Andrew, Susan
APPLICANT: Rowmens, Johanna M.
APPLICANT: Rowmens, Johanna M.
APPLICANT: Lin, Blaoyang
TITLE OF INVENTION: Passative of Huntington's Disease and Differential 3'
TITLE OF INVENTION: Polyadenylation in the Gene
NUMBER OF SEQUENCES: 14
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 1211 E. Morehead Street
CITY: Charlotte
STATE: No. 5534438th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Excepter, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3 Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 TITITITITITITITITITITITITITIGAGGGAGTCTTGCTCTGTCGCCCAGGCCGACT 280
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                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/126,587C FILING DATE: 24-SEP-1993 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Layton Jr., Samuel G.
REGISTRATION NUMBER: 22,807
REFERENCE/DOCKET NUMBER: 3477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704-377-1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOSOME/SEGMENT: 4p16.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                    : Hayden, Michael
                                         Goldberg, Paul
Andrew, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 380 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 60.6%
Matches 66; Conservative
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TELEFA: 704-374-2014
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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POSITION IN GENOME:
GENERAL INFORMATION:
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Gaps
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APPLICANT: Feder, John N.
APPLICANT: Feder M.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 40; DB 1; Length 1920;
63.5%; Pred. No. 0.061;
tive 0; Mismatches 35; Indels
                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/087,772A FILING DATE:
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ADDRESSEE: Bell, Seltzer, Park & Gibson STREET: Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                           3339-195
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08724394A Patent No. 5872237
         STREET: Post C. CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                     NAME: LINKET, RAYMOND O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-TELECHONE: 919-881-3140
TELEPHONE: 919-881-3175
INFORMATION FOR SEG 1D NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.5
Matches 61; Conservative
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69.2%; Pred. No. 1.5;
tive 0; Mismatches 24; Indels 0;
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APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: TSUchihashi, Zenta
APPLICANT: TSUCHIhashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587223
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 1.05/08/724,394A
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                017957-000100
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Patent No. 5872237
PC-DOS/MS-DOS
                                                                                                    CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179;
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: TWO EMECTION
OPERATING SYSTEM:
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Best Local Similarity
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0; Gaps
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1.7%; Score 39.6; DB 2; Length 246240;
Best Local Similarity 69.2%; Pred. No. 1.5;
Matches 54; Conservative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el TITLE OF INVENTION: Sequences and Antibodies Thereto NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/POCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                      017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08724394A Patent No. 5872237
                 REFERENCE/DOCKET NUMBER: 0179:
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Feder, John N. APPLICANT: Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
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STATE:
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RESULT 15
US-08-756-506-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                          1.7%; Score 39.6; DB 2; Length 246240; 69.2%; Pred. No. 1.5; ative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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1.7%; Score 39.4; DB 4; Length 2880;
Best Local Similarity 71.2%; Pred. No. 0.12;
Matches 52; Conservative 0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-115-284-3/C
Sequence 3, Application US/09115954B
Patent No. 5200776
GENERAL INCORATION:
APPLICANT: Boron, Walter F
APPLICANT: Bril, Antoine M
APPLICANT: Bril, Antoine M
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Control of APPLICANT: Avaing, Christopher J
APPLICANT: Brayling, Ch
                                                                                                                                                                                 : NAME/KEY: misc_feature
; LOCATION: 1..246240
; CTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-934A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09115954B Patent No. 6200776 GENERAL INFORMATION:
                                  STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95282 GGTCTCCAACTTCTGGGC 95299
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APPLICANT: Bril, Antoine M
APPLICANT: Khandoudi, Nassirah
APPLICANT: Martin, Xavier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1347 agtctcaaacttgcggtc 1364
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.7%
Best Local Similarity 69.2%
Matches 54; Conservative
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   nucleic acid
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; ORGANISM: Homo sapiens
US-09-115-954-3
                                                                                                                   CDNA
TYPE: nucleic STRANDEDNESS:
                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.7%; Score 39.4; DB Best Local Similarity 71.2%; Pred. No. 0.14; Matches 52; Conservative 0; Mismatches
                     APPLICANT: Rawlings, Christopher J
APPLICANT: Doe, Trudy R
TILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT FILLING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILLING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BAIL, Antoine M
APPLICANT: Bil, Antoine M
APPLICANT: Bil, Antoine M
APPLICANT: Martin, Xavier
APPLICANT: Jule, Steven C
APPLICANT: Salings, Christopher J
APPLICANT: Doe, Trudy R
ITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT APPLICATION NUMBER: EP97401714.7
EBALIER PILING DATE: 1998-07-15
EBALIER FILING DATE: 1997-07-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
APPLICANT: Jupe, Steven C
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                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-115-954-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-115-954-1
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us-09-445-201-1_copy_8336_10608.rni

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Sequence 1, Application US/08756506

Patent No. 5905185

GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Fronter, Cindy A.
APPLICANT: Prunkard, Donna E.
ITILE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: APPLICANT:
TITLE OF INVENTION: ANIMALS
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESSE: 24
COUNTRY: USA
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; ICCATION: join(3520..3630, 5093..5117, 5210..5347, 5450
; LOCATION: ..5584, 8253..8395, 9269..9386, 10516..11102)
US-08-756-506-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: June 21, 2001, 18:20:53 Job time: 17446 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELEPHONE: 206-442-6672
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11725 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                   1 tetegagacagageegetgt.....agggettteetattggatee 2273
                                                                                                                                                                                                          20456230
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                     10228115 seqs, 4726426750 residues
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                             US-09-445-201-1_COPY_8336_10608
2273
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Maximum Match 100%
Listing first 45 summaries
                                                - nucleic search, using sw model
                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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118 gbest49 **
119 gbest49 **
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123 gbest52 **
124 gbest52 **
125 gbest55 **
126 gbest56 **
131 gbest56 **
132 gbest60 **
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					STIMMA		IIII.
Result		e Onerv					JOUI
NO.	Score	Match	Length	DB	QI	Description	
н с	707	31	746	25	AZ815965	AZ815965 ZM0084D06	
v 60	79.2	7 (7	404	22	AC364007 AO126020	A236400/ IMULIUFU3 A0126020 HS 3032 B	
	78.6	m	464	22	AQ332669	AQ332669 HS_5004_A	
nν	2.92	7 (556 506	7 6	AZ508851	AZ508851 1M0351G04	
	55	10	256	13.	BE651040	BE651040 UI-M-BH3-	
	22	7	257	11	AW490147	AW490147 UI-M-BH3-	
	55	0 C	652	11	AW551517	AW551517 L0080A10-	
11	53.6	1 (432	7 7	A2423401 BF391061	BE391061 UI-R-CA1-	FEATU
	53.4		320	10	AI838610	AI838610 UI-M-AO0-	
	53.4	C) (429	23	A1661049	AI661049 mz78f09.x	
4 5	53.4	7 0	431	7 -	A18499/3 BE320748	AI8499/3 UI-M-BGU- BE300748 11755511 4	
	53.4	10	478	7	AA119334	AA119334 mp80e10.r	
17	53.4	7	631	12	AW826111	AW825111 us21h04.x	
	53	71 C	311	770	AZ306979	AZ306979 1M0008H17 AV102206 AV102206	
20	52.4	1 (7	652	24	AZ403474	AZ403474 1M0171B14	
	52.2	7	212	25	AZ913824	AZ913824 RPCI-24-1	
22	52	(7 (419	24	AZ637662	AZ637662 1M0497J12	
	51.0	4 C	4.58	22	AVU90924 AO355903	AVUSOSZ4 AVUSOSZ4 AO355903 CTTRT-E1-	
25	51.2	2 2	584	24	AZ750042	AZ750042 RPCI-24-8	
	51.2	~	621	24	AZ744458	AZ744458 RPCI-24-1	
27	51.2	(3 (631	24	AZ410081	AZ410081 1M0182G10	
9 0	20.02	4 (446	17	A1171758	AT171758 EST017740	
30	50.6	1 (2)	609	24	AZ791331	AZ791331 2M0041010	
31	50.4	7	311	24	AZ662311	AZ662311 1M0541N17	
	50.2	0.0	367	13	BE655196	BE655196 UI-M-BG1-	
0 KJ	50.2	1 C	384	4 4	A4316223 AA261578	A4316223 IMUU3/HU/ A4261578 mz87a12 r	
32	50.2	17	505	13	BE689422	BE689422 uw54d12.y	
	50.2	7	568	14	BF401678	BF401678 UI-R-CAO-	
37	50.2	~ (578	24	AZ762191 BE131067	AZ762191 1M0556L23	
	50.2	40	651	74	BF12109/ A2461771	BF12109/ 001/3/929	RAGE
	50	10	489	iH	AA004129	AA004129 mq82f03.r	ORIGI
	20	7	631	24	AZ431614	A2431614 1M0216G07	
42	49.8	(1)	396	15	4824	AI044824 UI-R-CI-k	
	4 4	70	5/5	243	2333030	A2393030 IMOISSUL9 A2615574 IMO445D12	one Ber
45	49.4	10	264	23	Z100588	AZ100588 RPCI-23-2	Mat
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					ALIGNMENTS		d.
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RESULT .	-						ολ
LOCUS		AZ815965	746 bp	dq	DNA		qa
DEFINITION		U84DU6R	Mouse 2M0084T	10kb	plasmid UUGCLM library Mus	fus musculus genomic	ò
ACCESSION		15965		2			~~
VERSION		AZ815965.1 GI:1298587	GI:12	9858	73		qq
SOURCE		house mouse	ė.				Oy
ORGANISM	_	Mus musculus Eukarvota; Metazoa;	us Metazc	. C		orata: Euteleostomi;	qq
a DNG GAGGA		Mammalia; Eutheria;	Eutheri	a; Re	Rodentia; Sciurognathi; Muridae	; Murinae	· č
AUTHORS		n, D., A	oyagi,#	, , Bi	ber, M., Beacorn, T.,	ral, B., Hamil, C.,	3
	ISI M	lam,H., L ., Rose,M	Longacre, M., Rose,	, s, s,	Mahmoud,M., Meenen,E Stokes,R., Tingey,A.	., Pedersen,T., Reilly , von Niederhausern,A.	qa
	and	3	. :	.SS, R			Qy

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)jplAFL29072.1), a copyrumber inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicible in resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                             SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1067 catctgtgttggtgagccagtggagaactgcctcctggctgttctcagaaggccacagtg 1126
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Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                      plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain=""c57BLf0"
/db_xref="taxon:10090"
/clone="uGC2M0084D06"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 746;
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98.4%; Pred. No. 1.1e-172;
Live 0; Mismatches 10;
                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0084 row: D column: 06
Seg primer: CACACAGGAAACAGGTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 746.
Location/Qualifiers
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                                                     URNAL
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TITLE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Agyagi. A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                     1546
                                                                                                                                                                                  E., SLC,
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0110F03"
/clone="UUGC1M0110F03"
/sex="Male"
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Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: F column: 03
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
High quality sequence stop: 586.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWM2 (gil47321141gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coil XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ126020 404 bp DNA GSS 23-SEP-1998
HS_3032_B2_C02_MF C1T Approved Human Genomic Sperm Library D Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tectttaccatggtgggcatgttacaggttagttgactgaaaactagttatetegetgtg 1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.7%; Score 560.8; DB 242; Length 586; 98.5%; Pred. No. 9.7e-135; live 0; Mismatches 8; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1877 tttcaggggtatggagacgagctgtagagagatgtctccagggag 1921
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1 (bases 1 to 404)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-coli DH10B"
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                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
sapiens genomic clone Plate=3032 Col=4 Row=F, DNA sequence.
AQ126020
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                                                                                                                                                                                                                                                                                                                                                                                                                        High Throughput Sequencing Center
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3032 row: F column: 4
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Location/Qualifiers
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                                                                AQ126020.1 GI:3503186
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                                          ACCESSION
                                                                                         KEYWORDS .
                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                 AUTHORS
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KEYWORDS
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1 (bases 1 to 464)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                On Feb 19, 1999 this sequence version replaced gi:4130296.
Contact: Mahairas GG, Wallace JC, Hood L
Contact: Mahairas GG, Wallace JC, Hood L
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3818
Fmail: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A2508851 556 bp DNA GSS 05-OCT-2000 MD351C9CR Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0351G04 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; RPCII1 Human Male BAC Library"
a 75 c 93 g 113 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1239 ggagtcatctgttcttagtcagtgcgaattagaaagcctggtggtgctgctattaat 1298
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                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GGAGTCATTTTTTTTTTGTTGATATGACTTAGAAAGCTTGGGTGCNTGCCCCACATCAAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.5%; Score 78.6; DB 227; Length 464; ilarity 66.5%; Pred. No. 1.4e-09; Conservative 0; Mismatches 62; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="plate=580 Col=17 Row=A"
/clone_lib="RPCI11 Human Male BAC Library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: SP6
Class: BAC ends
High quality sequence stop: 464.
Location/Oualifiers
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Mus musculus
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nes 125; Conserv
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Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                       Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-67J15.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Wale"
/cell_type="Spleen/Brain"
/cell_type="Spleen/Brain"
/note="Vector: pTakBaC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTakBaC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 506)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BE651040 GI:9976864
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                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
That Addical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/clone="RPCI-24-67J15"
/clone_lib="RPCI-24"
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1...506
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Seq primer: T7
                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gl4732114 gpl AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
daptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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RPCI-24-67J15.TV RPCI-24 Mus musculus genomic clone RPCI-24-67J15,
DNA sequence.
                                                                                                                                                                    SLC,
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                                                                                                                                                          308, Biomedical Polymers Research Bldg., 20 S. 2030 E., 12, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 2.6%; Score 58.2; DB 245; Length 556; Similarity 66.1%; Pred. No. 0.0003; 34; Conservative 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0351 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .556
/organism≂"Mus musculus"
                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0351G04"
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Best Local Similarity 66.18
Matches 84; Conservative
                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                    Email: mEST@mail.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
                                                                                                                                                                                                                                                               availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 52-169, >PBIDIO#SINE/Alu Seq primer: MI3 Reverse.
 1 (bases 1 to 256) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                         6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
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                                                                                          Contact: Chin, H
National Institute of Mental Health
                                                                                                                                                                                                                                                                                                                                                        /organism-"Mus musculus"
                                                         Genome Res. 6 (9), 791-806 (1996) 97044477
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Best Local Similarity 60.4.
Best Local 79; Conservative
                                                                                                                                                     Tel: 301 443 1706
Fax: 301 443 9890
                                               discovery
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AUTHORS
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/organism="muscutus".
/strain="GSTBL/6A"
/db_xref="taxon:10090"
/clone="unit build b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A strand cDNA and therefore this may represent a bonafide poly A and the sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence:
78-195, >PBDIO#SINE/Alu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BWAP_M_S4 library. This procedure has been previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 257)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                AW490147 257 bp mRNA EST 24-FEB-2000 UL-M-BH3-asy-e-08-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-asy-e-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Forward POLYA=Yes.
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Fax: 301 443 9890
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RESULT 8
AW490147/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 652)
Tanaka.T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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| Ab_xref="taxon:10090" |
| Clone="L0080All" |
| Clone_1lib="Mouse E12.5 Female Mesonephros and Gonads CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       AWS51517 652 bp mRNA EST 31-AUG-2000
L0080A10-3 Mouse El2.5 Female Mesonephros and Gonads cDNA Library
Mus_musculus cDNA clone L0080A10 3', mRNA sequence.
described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LISHH_BMAP_M_S4
TAG_TISSUB=10-brain-stems
TAG_SEQ-TCATG"
                                                                                                                                                                                                                                    1289 tgctattaattagttattcttcttctgagacagagtctcactgtgtggcccaggctag 1348
                                                                                                                                                                                                                                                                        1349 totcaaacttgcggtccatttgtctcactcatcagaatgctgggcttccaggtgtgtgc 1407
                                                                                                                                                                                                           Gaps
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0000 row: A column: 10
Seq primer: -2LM13 Forward
High quality sequence stop: 652
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                     Length 257;
                                                                                                                                                                                                       40; Indels
                                                                                                                                                                 Score 55; DB 116;
Pred. No. 0.0017;
0; Mismatches 40;
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/organism="Mus musculus"
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/lab_host="DH10B"
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Best Local Similarity
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free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Tag polywerse. Then, the cDNAs were purified by phenol/Chloroform and by Centricon 100. The cDNAs were digested with SalI and NotI enzymes. Then, the CDNAs were size selected by Gibco's Size Fractionation Column. The CDNAs were cloned into Sall/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Aiaohong Wang."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ423401 559 bp DNA GSS 03-OCT-2000 1M0202C02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0202C02 R, DNA sequence.
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/clone="taxon:10090"
/clone=lb="mouse l0kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 AAAGAAGATCTTACTATGTAGCCCAGGCTTGCCTTAAATGTGTGATCATCCTACCTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                           Query Match 2.4%; Score 55; DB 117; Length 652; Best Local Similarity 60.3%; Pred. No. 0.0021; Matches 108; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0202 row: C column: 02
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Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ423401.1 GI:10547414
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 432)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 TTTGAGGCAGGGTTTTGCTGTGTAGCCCCAAGCTGGCCTGTAACTTGCAGATCCCGTGTCT 439
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59.7%; Pred. No. 0.0023;
tive 0; Mismatches 62; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
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ORIGIN

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COMMENT

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/strain="Status Maryegicus"
/strain="Status Maryegicus"
/strain="Status Maryegicus"
/db_xref="taxon:10116"
/clone_11b="N-G-CA1-bcf-f-12-0-UI"
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/note="WetCAI: pT73D-pac (Pharmacia) with a modified
/note="WetCAI: Not I; Site_2: Eco RI; The UI-R-CAI
library is a subtracted library derived from the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
/midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized pineal glands library cDNA Library Preparation: M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 320)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 16-133, >PB1D10#SINE/Alu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1292 tattaattagttattettettettetgagacagagteteaetgtgtggeecaggetagtet 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIB38610 320 bp mRNA EST 14-JUL-1999 UI-M-AOO-abz-f-12-0-UI.S1 NIH_BMAP_MPG Mus musculus cDNA clone UI-M-AOO-abz-f-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1352 caaacttgcggtccatttgtctcactcatcagaatgctgggcttccaggtgtgtgc 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 GGAACTIGCTATCCTACTGTTCCAACCTCCAGAGTGCTGGGACTGAAGGTGTATTC 120
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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                                                                                                                                                                  /organism="Rattus norvegicus"
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                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_LIB=UI-R-CA1
TAG_TISSUE=medulla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_SEQ=GAACCG"
                                                       Seq primer: M13 Forward POLYA=Yes.
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AI838610.1 GI:5472823
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Fax: 301 443 9890
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SOURCE
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/strain="C57BL/64"
/db_xref="taxon:10090"
/clone="UI-W-A00-abz-f-12-0-UI"
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/clone="UI-W-M-MO"
/clone="Nost="NIH BMAP_MPG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH BMAP_MPG library is a non-normalized library
constructed from mouse pineal gland. The tag is a string
of 5 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
/loc-Miller Laboratories.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 1-44, >AT_rich#Low_complexity 103-204, >PBIDIO#SINE/Alu POLYA=YES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mz78f09.x1 Soares mouse NML Mus musculus cDNA clone IMAGE:719561 3' similar to SW:RFXA_HUMAN 000287 REGULATORY FACTOR X-ASSOCIATED PROTEIN ;, mRNA sequence.
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The Washu-NCI Mouse EST Project 1999

Other_ESTS: mz78f09,yl
Contact: Marra Mymshu-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53.4; DB 102; Length 320; Pred. No. 0.0046;
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                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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TAG_TISSUE=pineal-glands
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Best Local Similarity 69.9%;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 431) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
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National Institute of Mental Health
National Institute of Mental Health
2001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 2.3%; Score 53.4; DB 23; Length 429; Best Local Similarity 69.9%; Pred. No. 0.0049; Matches 72; Conservative 0; Mismatches 31; Indels 0.
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                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
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/lab_host="DH10B"
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/clone_lib="Now_arm.vert"/
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Email: cgapbs-remail.nih.gov
Tissue Procurement. Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)

DNA Sequencing by: Washington Gniversity Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 1-41. >AT_rich#LOW_complexity 100-201, >PBIDIO#SINE/Alu POLYA-Yes.
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NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES

		Description	00000000 FC1000X8	1000 to 170000	AF061804 Mus muscu	AF153058 Mus muscu	AC019251 Homo sapi	AC021220 Homo sapi	AC013745 Homo sapi	AF327424 Arabidops	AC007659 Arabidops	
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Breider, G. and Risau, W.
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MAX PLANCK GESELLSCHAFT (DE); BREIER GEORG (DE)
Location/Qualifiers
1. .12845
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Best Local Similarity 100.0%; Pred. No. 3.3e-154;
Matches 515; Conservative 0; Mismatches 0;
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/db_xref="taxon:32644"
2893 c 2863 g 3723
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AC026659
AC016759
AF064258
HSDJ685D6
AC079069
                                            AF217246
AL390758
HSJ1059A9
AL162731
                  AC079086
AC010103
AP003265
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AC009475
AC009956
HS21C079
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AC068355
AF159056
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AL391987
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AC013763
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AL138761
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6.7 183575
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Mus musculus
Eukaryota; Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 510)
Kappel,A., Ronicke,V., Damert,A., Flamme,I., Risau,W. and Breier,G. Identification of vascular endothelial growth factor (VEGF)
receptor-2 (Flk-1) promoter/enhancer sequences sufficient for annyioblast and endothelial cell-specific transcription in transgenic mice
Blood 93 (12), 4284-4292 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (28-APR-1998) Molekulare Zellbiologie, Max Planck
Institut fuer physiologische und klinische Forschung, Parkstrasse
1, Bad Nauheim 61231, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus fetal liver kinase 1 (Flk1) gene, intronic enhancer.
AF061804
AF061804.1 GI:5757676
23-AUG-1999
                                                                                  teaggggtatggagacgagetgtagagagatgtetecagggagtttteattaateageaa
                                                                                                                                                                tttagtcagatctgtgcatcctatgctttacaagaaatgtcagtgggcctgagatcatca
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Kappel, A., Roenicke, V., Damert, A., Flamme, I., Risau, W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10574 TGCATTGTTTATGGAAGGCTTTCCTATTGGATCC 10608
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/strain="C57BL"
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/gene="Flk1"
/note="intronic"
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/gene="Flk1"
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REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Appel,A., Risau,W. and Breier,G.

Prerequisite role of SCL/tal-1, GATA and Ets transcription factor

binding sites for the in vivo function of F1k-1 gene regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-WAY-1999) Molecular Cell Biology, Max-Planck,
Institut fuer Physiologische und Klinische Forschung, Parkstrasse
1, Bad Nauheim 61231, Germany
                                                                                                                                                                                                                                                                                                                                                                                       303 caggaaaacaggaactccaccctggtgcgtgaattgcagagctgttgtgttgttgtg
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                                                                        Gaps
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Mus musculus tyrosine kinase FLK-1 minimal enhancer sequence.
AF153058
                                                                                             taaatgtgctgtctttagaagccactgcctcagcttctgcagctcagataccaaaggaag
                                                                                                          1 TAAATGTGCTGTCTTTAGAAGCCACTGCCTCAGCTTCTGCAGCTCCAGATACCAAAGGAAG
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                                              Length 510;
                                                                      Indels
                                             99.0%; Score 510; DB 94; 1
100.0%; Pred. No. 8.7e-153;
iive 0; Mismatches 0;
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Direct Submission
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 131
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2 (bases 1 to 430)
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Best Local Similarity 100.
Matches 510; Conservative
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BASE COUNT
                                                                                                                                                                                                                                                                                          243
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TITLE
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JOURNAL
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AF153058
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/db_xref="taxon:10090"

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barran, N., Beckerly, R., Bada, F., Colayandin, J., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Poyle, M., Fensestor, J., Garestor, J., Gereira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
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Homo sapiens chromosome 4 clone RP11-5E20 map 4, LOW-PASS SEQUENCE
SAMPLING.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135552)
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                                                       /note="tyrosine kinase FLK-1 minimal enhancer"
94 c 112 g 116 t
                                                                                                                                                                                             Length 430;
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                                                                                                                                                                                       83.5%; Score 430; DB 94; L
100.0%; Pred. No. 4.5e-127;
iive 0; Mismatches 0;
/dev_stage="fetus"
1. .430
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HTG; HTGS_PHASE0.
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Matches 430; Conservative
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COMMENT

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Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                       Jilitai, A. and Zody, M.

Jimmer, A. and Zody, M.

Direct Submission
Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 5, 2000 this sequence version replaced 9::6649482.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                  * NOTE: This record contains 153 individual

* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
voverlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                         Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: 1.2005
Center clone name: 5_E_20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              752: contig of 752 bp in length 852: gap of 100 bp 1137: contig of 785 bp in length 1137: gap of 100 bp 2506: contig of 769 bp in length
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86 bp in length
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100 bp
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1478: contig of 732 bp in length
58; gap of 100 bp
15655: contig of 797 bp in length
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14027 14758; cont
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3392: con
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10374: con
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18 32417; gap of 1700 bp in length 3198; contig of 781 bp in length 3298; gap of 100 bp a 34081; contig of 783 bp in length 34081; contig of 783 bp in length 100 bp a 34938; contig of 787 bp in length 100 bp a 35795; contig of 757 bp in length 100 bp a 35795; contig of 757 bp in length 100 bp a 35624; contig of 757 bp in length 100 bp a 35795; contig of 777 bp in length 100 bp a 35795; contig of 777 bp in length 100 pp a 3775; contig of 774 bp in length 100 pp a 3775; contig of 774 bp in length 100 pp a 3775; contig of 774 bp in length 100 pp a 38375; contig of 774 bp in length 100 pp a 38375; contig of 774 bp in length 100 pp a 38375; contig of 774 bp in length 100 pp a 38375; contig of 774 bp in length 100 pp a 38375; contig of 774 bp in length
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f 789 bp in length
100 bp
f 784 bp in length
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contig of 790 bp in length
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contig of 789 bp in length
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contig of 797 bp in length
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47981: contig of 791 bp
100 bp
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f 762 bp
                                  19183: contig of 774 bp
19283: gap of 100 bp
20038: contig of 755 bp
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49724: contig of 757 bp
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19183; cont
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20878: con
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25313: con
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27045: con
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32317; con
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39264: con
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44507: con
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                                                                                                                                                                                    20978: gap of
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Direct Submission
Submitted (15-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Nov 15, 2000 this sequence version replaced gi:9309528.
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 214348)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
         Homo sapiens chromosome 4 clone RP11-530117, WORKING DRAFT SEQUENCE, 38 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 161000; agarose-fp
Insert size: 210648; sum-of-contigs
Quality coverage: 4.96 in 020 bases; agarose-fp
Quality coverage: 4.62 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 12236 bp in length
unknown length
of 13128 bp in length
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unknown length
of 22038 bp in length
unknown length
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length
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of 9967 bp in length
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of 9080 bp in length
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length
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contig of 2510 bp in len
app of unknown length
contig of 2130 bp in len
gap of unknown length
contig of 3320 bp in len
gap of unknown length
contig of 4157 bp in len
gap of unknown length
gap of unknown length
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79.0%; Pred. No. 2e-86;
tive 0; Mismatches 94; Indels 17; G
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49824: gap of 100 bp
50586: contig of 762 bp in length
5686: gap of 100 bp
51456: contig of 770 bp in length
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                                      72963. .66090 "-

/note="assembly_name:Contig109"

66191. .82659 "-

/note="assembly_name:Contig110"

82760. .104797 /-

/note="assembly_name:Contig111"
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177767. .178997. note="assembly_name:Contig37"
179098. .180242. /note="assembly_name:Contig56"
180343. .181442
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197845. .199489

/note="assembly_name:Contig90"

199590. .201304

201405. .203316

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203417. .20490
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182743. 184165_nome:Contig69"
/note="assembly_name:Contig69"
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185613. 187121
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187222 . 188524
100te="assembly_name:Contig78"
188625 . 189782
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189883 . 191312
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194218. .195948

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129420. 176511
/note="assembly_name:Contig113"
176612. 177666
                                                                                                                                      note="assembly_name:Contig112"
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note="assembly_name:Contig105"
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/note="assembly_name:Contig107
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gap of unknown l
contig of 2151 k
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
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Dipublished

Baldwin, J., Barnana, N. Beckerly, R., Boqualavky, L., Boukhgalter, B.,

Baldwin, J., Barnana, N., Beckerly, R., Boqualavky, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangolo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., Fitzlugh, M., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Suy, A., Sartos, R., Severy, P.,

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Li Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:6910837.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 4 clone RP11-92P18 map 4, LOW-PASS SEQUENCE SAMPLING.
                                  Db 100502 GAGTGAGATCATCAGATGAAGGTTCATTGGTTTCAATGTCCCGTATCCTTTTGTAAGAC 100443
                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 126330)
                                                                                                                                                                                                                                                                                                                                                                                               DD 100322 TACTGAGAATGGTGAAAAGTAAATTCCCAGTTTTATACAATGAATTGCTGAAGAGGCCTT 100263
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Center: Whitehead Institute/ MIT Center for Genome Research
      ---tgagatcatcagatggaggttcatcgggtttcaatgtcccgtatccttttgtaagac
                                                                                                                                                                                                                                                                                                                                                            407 aactgggactggggcaaagtcaa-tcccacctttatacaatgaattgctgaagaggcctt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This record contains 147 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
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------- Project Information
Center project name: L2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-92P18 Unpublished
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                          overlap relationships among clones to be deduced.
However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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5 9827: contig of 7
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41985: contig of 749 bp in length
185: gap of 100 bp
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115: gap of 100 bp
43632: contig of 717 bp in length
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54329: contig of 713 bp in length
contig of 702 bp
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40316: contig of 690
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47765: contig of
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51884: contig of
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52702: contig of
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Arabidopsis thallana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eddicotyledons; core eddicots; Rosidae; eurosids II;
Magnollophyta; eddicotyledons; core eddicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 847)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Bavis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                   5;
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Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, K., K., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,
                                                                                                                                                                                                                                              AF327424 847 bp mRNA PLN 26-FBB-2001
Arabidopsis thaliana unknown protein (T14P1.19/At2g45010) mRNA,
partial cds.
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                                                                                                                                                                                                        aggaagtetiggtacacagcatgataaaagacaatgggaeggggteacagtggeteeegte 116
                                                                                                                                                                                                                                                                                                                                                                                                                                              230 -----tgagatcatcagatgaggttcatcgggtttcaatgtcccgtatccttttgta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agctgttgttgttgttgttgtgaccatctgccattcttcctgttatgacagagcttgtgaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 126330;
  57728: gap of 100 bp
58523: contig of 795 bp in length
58623: gap of 100 bp
59387: contig of 764 bp in length
                                                                                                                         DB 63;
                                                                                                                     Score 254.4; DB 63;
Pred. No. 2.8e-70;
0; Mismatches 144;
                                                                                   100 bp
57629 57728: gap of
57729 58523: conti-
58524 58623: gap of
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FLI_CDNA.
thale cress.
                                                                                                                                          Best Local Similarity 66.4%;
Matches 314; Conservative
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ECMQVLPETYEPPSDENWTTGIFGCAEDPESCRTGLFCPCVLFGRNIEAVREEIPWTQ
PCVCHAVCVEGGMALAAVTALFSGYIDPQTTVVICEGLFFAWWGGIYSGLFRQELQR
YHLKNAPCDHCMVHCCLHWCALCOEHREMKNHLSDTEASSSTTMDPPPVQENNTEER
RDASSSSSSPSSAKSQHNA
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                                         Submitted (11-DEC-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seti,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RAFL3-4-K9 (R09069)"
/note="This clone is in pBluescript vector as a XhoI/SstI
                                                                                                                                                                                                                            The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAS: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Ouach,H.L., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 cagatctgtgcatcctatgctttacaagaaatgtcagtgggcctgagatcatcagatgga 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana chromosome II section 241 of 255 of the complete sequence. Sequence from clones Il3E15, T14P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.7%; Score 39.4; DB 13; Best Local Similarity 71.2%; Pred. No. 0.19; Matches 52; Conservative 0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thallana"
/db_xref="taxon:3702"
/chromosome="2"
Davis, R.W., Ecker, J.R. and Theologis, A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=experimental
/product="unknown protein"
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/db_xref="G1:11935197"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="T14P1.19/At2g45010"
134. .>847
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1. .>847
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AC007659/c
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KEYWORDS
SOURCE
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                        TITLE
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetplantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TiGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan SE (Sean Eddy,
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicaceae; Arabidopsis.

I (bases 1 to 87885)
Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.Y., Bell,C.R., Ketchum,K.A., Lee,J.J., Roning,C.M., Foo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing enclose F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bloinformatics Department, especially Lixin Zahou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:4895233.
The sequence and annotation of chromosome 2 were merged from those
of the individual clones on this chromosome after removing
overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This work was supported by the National Science Foundation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     numbered from the top to bottom of the chromosome.
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/note="Sequence from clone T13E15"
complement(2902. .>87885)
/note="Sequence from clone T14P1"
2904. .>3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Address all correspondence to: at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .87885
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.tigr.org/tdb/at/at.html).
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/chromosome="II"
complement(<1, 2901)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter, J.C.
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complement join(<18068. .18186,18313. .18477,18558. .18703, 18775. .19400,19477. .19602,19724. .19924,20006. .20113, 20188. .202587,20397. .20514,20614. .20749,20875. .21046, 21269. .21400,2151. .21684,21782. .21871,22075. .>22297))
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MISTRAGGYGLNLVAADŢVIFYEQDWNPQVDKQALQRAHRIGQISHVLSINLVTEHSV
ESTILRRAERKLQLSHWYGDNMEEKEBDGGDLRSLVFGLQRFDPEETHWESDNLKM
VEISSLAEKYVAIROWVEDVERRREINSDTLLGMTSSAĞLDSELDEASYLSWVEK
KKEAARSSKDEKIIELGNRKNLSEERNLRIEAARKKAEEKKLAŢWGAHGYQSLSVEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPPVEDGTDRFNKILEDIGNHGPLYFVDTKTKFSKMGLACHIAKIHSESSVEKNAREI
KEYIEELCWGSNKRVLLLGHSKGGIDAAAALSLYWPELKDKVAGLVLAQSPYGGSPIA
TDILREGQLGDYVNLRKMMEILISKVIKGDIQALEDLTYERRKEFLKNHPLPRELPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"SNF2 subfamily global transcription activator" protein_id="AAD32837.1" | Protein_id="AAD32837.1" | Protein_id="AAD3282" | Abox xref="GI:4895252" | Abox xref="GI:
                                                                                                                                                                                                                                                                                                                                                                           TQATSYLGSLEYGGKDTISHPHELLRSTSGVDGNSPVSVCISPGERFSTSSEASTSDA
NSPSRESTEILPQATNAIVTSNRLNLNGISMFQGLIERARRTVRGSADDIGWLQRAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFRTEAS ISPAVLSTLSHVAHAELPLTNQAAKLPVVMPLGAAMAACAQLLQVRYGEKS
DGLVTCCDAEVPGSVVVRPKRKLDHAMMVYSSLNEVPLEADAAQVCEALLTLLVQVEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGVTATLKPHOVEGVSWLIOKYLLGVNVVLELDOMGLGKTLQAISFLSYIKFROGLPG
PFLVLCPLSYYDGWYSEINRTPNLEYLRYVGDKYCRLDMKSMYDHGBFLPFDVLLT
TYDIALVDQDFLSQIPWGYRIDBAGRLKNPNSVLXNVLLEGFLIPRLLITGFPIQN
NLTELMALMHPCMPLVPGTLDOPLSAFKETGDGLDVSNNKETYKELKFILGAFMLRRI
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IVIQLRKACSHPYLFPGIEPFPFEFGEHLVQASGKLLVLDQLLKRLHDSGHRVLLFSQ
                                                                                                                                                                                                                                               /protein_id="AaD32838.1"
/db_xref="GI:4895253"
/translation="MGEAGQSRDGESVTPLVGGGNGDNAVAPQVFNSLPALNEAASYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(18068. 18186,18313. 18477,18558. 18703, 18775. 19400,19477. 19602,19724. 19924,20006. 20113, 20198. 20287,20397. 20514,20614. 20749,20875. 21046, 21159. 21699. 21400,21551. 21684,21782. 21871,22075. 22297))
/note="T14P1.23; identical to GB:AAC31827"
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15955. .161123,16289. .16535,16728. .16836,17072. .17122))
/gene="At2g44970"
/note="unknown protein"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 196646)
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Mus musculus chromosome 1 clone RP23-181N5, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL365329.6 GI:11863425
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement <18068. .>22297)
/gene="At2g44980"
/note="T14P1.22"
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9035. .9172,9411. .9497,9590. .9662,9774. .9968,10342. .10418,
10632. .10703,10786. .10946,11037. .11255,11310. .11343))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement join (<8230. 8361,8487. 8652,8747. 8949,
9035. 9172,9411. 9497,9590. 9662,9774. 9968,10342. 10418,
10632. 10703,10786. 10946,11037. 11255,11310. >11343))
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/gene="At2g44970"
/gene="At2g44970"
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13417. .13578.13759. .>13875))
/gene="At2g44960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSSTNSNFIEEDNSKRASRRSLSSLVSVEDDDDQNGGGGKRRTNGGDKHPTYRG
VRMRSWGKWVSEIREPRKKSRIWLGTYPTAEWAARAHDVAALAIKGTTAYLMFPKLAG
ELPRPVTNSPKDIQAAASLAAVNWQDSVNDVSNSEVAEIVEAEPSRAVVAQLFSSDTS
TTTTTQSQEYSEASCASTSACTDKDSEEEKLFDLPDLFTDENEMMIRNDAFCYYSSTW
QLCGADAGFRLEEPFFLSE"
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/db_xref="G1:4895255"
/translation="MALLEKLQVISVVKLSSIRKFQVEKDSIVWKEREINIKNELGDV
SRKTSAVTDSRMASLDSEIQKQLDEKMRIKTRLGNISRERGRKEIFADMKALISSFPE
EMSSMRSQLNNYKETAGG1HSLRADVOSLSGVICKRYRKEYEALQLRSADYASQLGDLN
ATVCDLKNSHEELKLFLDMYKRESTDARDIAEAKEQEYRAWAHVQSLKSSLDEQNLEL
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QTIGSAYEDIVPQNQQLLLQVTERDDYNIKLFLEGITSRQMQDTLLIDKYIMDKDIQQ
GSAYASFLSKKSSRIEDQLRFCTDQFQKLAEDKYQKSVSLENLQKKRADIGNGLEQAR
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                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MARQINIESSVSQVTFISSAIPAVSSSSSITASASLSSSPTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKLRQELSEFKEILKCKACNDRPKEVVITKCYHLFCNPCVQKLTGTRQKKCPTCSASF
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13417. .13578,13759. .13875))
/gene="At2g44960"
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                                                                                                                                                                                                                                                                                              /product="putative AP2 domain transcription factor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDVLVKFKSLSRELQSHRDADAKVRVDLKRIRGSYLVSSHSTIYC"
                                                                                                                            /note="T14P1.26; pFAM domain (PF00847)"
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/gene="At2g44960"
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complement(<8230, .>11343)

/gene="At2944950"

/note="T14P1.25"
                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD32841.1"
/db_xref="G1:4895256"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2972, .3067)
/rpt_family="(GGA)n"
6558. .6661
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complement(6771. 6870)
/rpt_family="(TAAAA)n"
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/note="unknown protein"
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/rpt_family="(TAAAA)n"
                                          2904. .>3809
/gene="At2g44940"
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    'gene="At2g44940"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 259487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 107247 GAGAFATGTTTAGAGGCATTTAGATTTTTCAGTCATTTTAGACACTTTGTGTTATTT 107306
                                                                                                                                                                                                Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
Conterproject Information
Center project name: buildln5
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: LOB752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 196518 bases at least Q40
Consensus quality: 196567 bases at least Q30
Consensus quality: 196587 bases at least Q20
Insert size: 196646; sum-of-contigs
Insert size: 196403; 4.3% error; agarose-fp
Quality coverage: 15.20x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 107307 TACCTCCAAGTATTACCTGTGATCCTTACAATAACTGAGCAATTTCCAGCAGTTCTAATG 107366
                                      Submitted (03-MAR.2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 15, 2000 this sequence version replaced gi:11691743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 gagagatgtctccagggagttttcattaatcagcaatttagtcagatctgtgcatcctat 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 gctttacaagaaatgtcagtgggcctgagatcatcagatggaggttcatcgggtttcaat 264
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Mus musculus chromosome 1 clone RP23-282D4, *** SEQUENCING IN
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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a 39346 c 40064 g 63964 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP23-181N5"
/clone_lib="RPCI-23"
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                                                                                                                                                                                    Center code: UK-MRC
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Lovell, J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
Mus musculus
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JOURNAL
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AUTHORS
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SOURCE
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                                                                                                                 COMMENT
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Db 250707 GAGATATGTTTAGAGGCATTTAGATTTTTTCAGTCATTTTAGACACTTTGTGTTATTT 250766
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Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 259474 bases at least 040
Consensus quality: 259487 bases at least 020
Insert size: 259487; sum-of-contigs
Insert size: 243892; 2.4% error; agarose-fp
Quality coverage: 15.92x in 020 bases; sum-of-contigs Quality
coverage: 17.27x in 020 bases; agarose-fp
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16229)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Direct Submission
Submitted (03-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1854, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Feb 10, 2001 this sequence version replaced gi:12666279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 gagagatgtctccagggagttttcattaatcagcaatttagtcagatctgtgcatcctat 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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56712 c 56734 g 75694 t
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                                                                                                                                                                                                                                    Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
Project Information
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/organism="Mus musculus"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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REFERENCE

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/note="assembly_fragment"
17535. .19935
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64814: cont
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                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bartei, C., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHogh, W., Gage, D., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Lamazares, R., Landers, T., Lehoczky, J., Levine, K., Lieu, C., Liu, G., Macdonald, P., Marquis, N., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., McEwan, P., McRernan, K., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivar, T.M., Oliver, J., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Yasailev, H., Viel, R., Vo, A., Zinmer, A. and Zody, M., Trigilio, J., Young, G., Zainoun, J., Zinmer, A. and Zody, M., Tavers, M., Trigilio, J., Young, G., Zainoun, J., Direct Subrission, Direct Subrission, M., Yasailev, H., Viel, R., Vo, A., Direct, Subrission, M., Yasailev, H., Viel, R., Vo, A., Direct, Subrission, M., Yasailev, H., Viel, R., Vo, A., Direct, Subrission, M., Yasailev, H., Viel, R., Vo, A., Mand, M., Man, D., Ye, W., Yaman, J., Yasailev, H., Viel, R., Vo, A., M., M., M., M., M., W., Waman, D., Ye, W., Yaman, J., Yasailev, M., Yanan, J., Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 18, 2000 this sequence version replaced gi:9845128.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 70_M_19

Sequencing vector: Plasmid; now, 100% of reads

Sequencing vector: Plasmid; now, 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 149171 bases at least Q40

Consensus quality: 155807 bases at least Q20

Consensus quality: 158244 bases at least Q20

Insert size: 163000; agarose-fp

Insert size: 154999; sum-of-contigs

Quality coverage: 3.7 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L10622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1089 1188: gap of 100 bp 1189 2239: contig of 1051 bp in length 2240 2339: gap of 100 bp 3811: contig of 1472 bp in length 3812 3911: gap of 100 bp 100 bp 3912 5158: contig of 1247 bp in length
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   sapiens chromosome 4, clone RP11-70M19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                (bases 1 to 162299)
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COMMENT

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102852 102951: gap of 100 bp
102952 114380: contig of 11429 bp in length
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126923 141300: contig of 14378 bp in length
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                                                                                                                                                                               27493: gap of 100 bp 47629: contig of 20136 bp in length 47729: gap of 100 bp 51364: contig of 3635 bp in length
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13127 15329: contig of 2203 bp in length
15330 15429: gap of 100 bp
15430 17434: contig of 2005 bp in length
                                                        17435 17534: gap of 100 bp
17535 19935: contig of 2401 bp in length
19936 20035: gap of 100 bp
20036 23899: contig of 3864 bp in length
                                                                                                                                         p of 100 bp contig of 3394 bp in length
                                                                                                                                                                                                                                                                      977: contig of 4513 bp in length
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88042: contig of 6388 bp in length
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contig of 7147 bp in length
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1. .1088
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
/chromosome="4"
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2 (bases 1 to 194038)
Waterston R.H.
Direct Submission
Submitted (11-Sip-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                               Direct Submission
Submitted (24-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki,T., Matsumoto,T. and Yamamoto,K.
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Cloyas astiva nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0490D09
Bublished Only in DataBase (2001) In press
2 (bases 1 to 157721)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (19-FBB-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 194038) Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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On Mar 24, 2001 this sequence version replaced gi:11597168.
Center project name: H_NH0508H21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 194038;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-508H21"
65587 a 34664 c 32553 g 61234
                                                        The sequence of Homo sapiens clone Unpublished
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HTG; HTGS_PHASE2.
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Waterston, R.H.
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Homo sapiens clone RP11-508H21, complete sequence.
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/note="assembly_fragment"
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2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakidabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs
NOTE: It currently consists of 1 contigs. Gaps between the correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* This is a 'working draft' sequence.
* This sequence will be replaced
* This had sequence as soon as it is available and
* the accession number will be preserved.

* The accession number will be preserved.
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Taudien, S., Blechschmidt, K., Menzel, U., Polley, A., Reichwald, K., Rump, A., Schilhabel, M.B., Schudy, A., Wen, G. and Rosenthal, A.
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Taudien, S., Blechschmidt, K., Menzel, U., Polley, A., Reichwald, K., Direct Submission
Submitted (05-SEP-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany.
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany.
On Sep 5, 2000 this sequence version replaced gi:8152189.
* NOTE: This is a 'working draft' sequence. It currently
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Baumgart,C. and Rosenthal,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 83; Length 157721;
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0; Mismatches
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/organism="Oryza sativa"
/cultivar="Nipponbare"
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56.0%; Pred. No. 3
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AF217246.4 GI:9967152
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Best Local Similarity 56.09
Matches 70; Conservative
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consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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88176: contig of 18001 bp in length
88276: gap of 100 bp
90769: contig of 2493 bp in length
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/note="assembly_fragment:00232
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/note="assembly_fragment:01164"
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/note="assembly_fragment:00401"
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/note="assembly_fragment:00466"
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/note="assembly_fragment:00571"
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/note="assembly_fragment:00907"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148267)
                                                                                                                                                                                                                                                                             Homo sapiens chromosome 10 clone RP11-540C21, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 1.08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 136465 bases at least 040
Consensus quality: 141338 bases at least 040
Consensus quality: 144184 bases at least 020
Insert size: 146567; sum-of-contigs
Insert size: 146541; 2.3% error; agarose-fp
Quality coverage: 3.2x in Q20 bases; sum-of-contigs Quality
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COMMENT

2005 others vector_side:right" 44012 a 29271 c 28195 g 44784 t BASE COUNT ORIGIN

0; 0; Gaps Query Match 7.1%; Score 36.8; DB 81; Length 148267; Best Local Similarity 56.7%; Pred. No. 2.6; Matches 68; Conservative 0; Mismatches 52; Indels 0; 0 Search completed: June 21, 2001, 18:37:34 Job time: 18633 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Mouse endothelial	Arabidopsis thalia	Arabidopsis thalia	Stealth virus nucl	N. meningitidis pa	Neisseria meningit	N. meningitidis B	Arabidopsis thalia	Human secreted pro	Human ORFX ORF1944	E. coli J96 pathog
SUMMARIES			ID	1									C76389	V31227
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	17	30	80	8882	-	236321	Mechanical stress
	18	29.8	œ.	550	_	C52708	Arabidopsis thalia
O	19	29.8	œ.	1590	_	Z99655	DNA coding for the
	20	29.8	æ	2105	Ξ.	C59480	secreted
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υ	22	29.6	۲.	308	_	C16102	
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/note= "DNA sequences comprising nucleotides 8260-10560, 8336-10608 and/or 10094-10608 are specifically claimed in Claim 3b" 10137..10155 /*tag= d /note= "GATA/PEA3 consensus binding site" Location/Qualifiers 6036..6959 /*tag= a 6661..7026 /codon_start= 6960 7027..10632 /*tag= b /number= 1 U /*tag= c /number= protein_bind promoter Mus sp intron exon Key

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This 12.8 kb DNA sequence spans the region from -6.65 kb relative to the transcriptional start site to +6.15 (located in the third exon) of the murine endothelial growth factor (VEGF) receptor-2 gene of the murine endothelial growth factor (VEGF) receptor-2 gene of the murine endothelial growth factor (VEGF) receptor-2 gene of mouse strain 129/SvJ by screening a phage library of liver of mouse strain 129/SvJ by screening a phage library of liver genomic DNA in vector lambda FixII. Sequences within the 5'-flanking region of the gene, in combination with sequences located within the first intron, specifically and reproducibly target expression of heterologous DNA to angloblasts during early stages of vascular experiences of the first intron also function as an autonomous andothelium-specific enhancer when fused to autonomous endothelium-specific enhancer, This Fix-1 intron enhancer contains several potential binding sites for transcription factors of the Ets and GATA families. The invention provides a contained recombinant DNA (I) comprising at least one regulatory sequence from an intron of the Fix-1 gene, or its homologue, to control expression in endothelial cells, in vivo, linked to (b) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA containing heterologous sequence controlled by endothelial cell specific regulator - from the Flk-1 gene, used to treat, prevent or diagnose vascular disease, tumours, also to screen for transcriptional regulators
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99US-0139763.
99US-0139817.
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99US-0129845.
99US-0130077.
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99US-0135353.
99US-0135629.
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99US-0137528.
99US-0137502.
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99US-0138094.
99US-0138540.
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99US-0139119.
99US-0139452.
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99US-0139492.
99US-0139454.
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99US-0123548,
99US-0125788,
99US-0126264.
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99US-0127462.
99US-0128234.
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99US-0134370.
99US-0134768.
99US-0134941.
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99US-0136392.
99US-0136782.
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99US-0139463
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99US-0140695
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
01-APR-1999;
06-APR-1999;
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06-MAY-1999;
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11-MAY-1999;
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19 - MAY - 1999
20 - MAX - 1999;
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25 - WAY - 1999;
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01 - JUN - 1999;
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21-JUN-1999;
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08-JUN-1999;
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18-JUN-1999;
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       EP1033405-A2
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23-JUN-1999;
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01-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990S-0153758.
990S-0154018.
990S-0154779.
990S-0155139.
990S-0155486.
990S-0155486.
990S-0155486.
990S-0157137.
990S-015833.
990S-015833.
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990S-0159637.
990S-0159584.
990S-0160741.
990S-0160768.
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99US-0160814.
99US-0160815.
99US-0160980.
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990S-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
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99US-0159329.
99US-0159330.
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99US-0162142
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28-0CT-1999;
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29-OCT-1999;
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Best Local Si
Matches 52;
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/mote= "this nucleotide is represented as a * in the
specification, and is included to maintain the
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21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stealth virus nucleic acid clone, SEQ ID NO: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
2196
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         990S - 0154779
990S - 0155486
990S - 0155486
990S - 0155659
990S - 0157117
990S - 0157117
990S - 0157865
990S - 0157865
990S - 0157865
990S - 015923
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990S - 0159330
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990S - 0160767
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    20. SEP-1999; 22. SEP-1999; 24. SEP-1999; 24. SEP-1999; 24. SEP-1999; 24. SEP-1999; 25. SEP-1999; 25. SEP-1999; 25. SEP-1999; 26. SEP-1999; 26
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990S-0142154.
990S-0142390.
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990S-0142803.
990S-0142977.
990S-0143542.
990S-014400S.
990S-014400S.
990S-0144086.
990S-0144086.
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99US-0144333.
99US-0144334.
99US-0144335.
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99US-0144884.
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99US-0147493.
99US-0147935.
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99US-0149723.
99US-0149929.
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990S-0151065.
990S-0151080.
990S-0151303.
990S-0151438.
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99US-0146386.
99US-0146388.
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99US-0153758.
99US-0154018.
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99US-0145218
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99US-0145919
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99US-0147303
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99US-0147038
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99US-0150566
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99US-0148341
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23 - AUG - 1999

24 - AUG - 1999

25 - AUG - 1999

26 - AUG - 1999

27 - AUG - 1999

28 - A
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Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.

Neisseria meningitidis.

WO200022430-A2.

N. meningitidis partial DNA sequence gnm_21 SEQ ID NO:21.

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invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nuclectide. The method comprises the steps of: (a) isolating DNA or RNA from a sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopethic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 or more contiguous nucleotides identical to sequence previously cr more contiguous nucleotides identical to sequence previously contained from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA molecules that react with the probe. The method is used to detect stealth virus in a biological product, food or in the inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                                   b "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
base numbering given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a Stealth virus nucleic acid clone. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2274 BP; 706 A; 375 C; 266 G; 769 T; 158 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 68-69; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel strains of stealth virus
                                                                                                                                                                                                                      98WO-US27744.
                                                                                                                                                                                                                                                         97US-0001184
                                     /*tag=
/note=
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-405521/34.
                                                                                                                                                                                                                                                                                                (MART/) MARTIN W J.
                                                                                                                                                                                                                                                         30-DEC-1997;
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                                                                                                                                                                                                                      30-DEC-1998;
                    misc_feature
                                                                                                                                                                                                                                                                                                                                        Martin WJ;
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Scarlato V;

Tettelin H, Venter JC; Ratti G, Scarselli M,

Frazer CM, Hickey E, Peterson J, Masignani V, Galeotti C, Mora M,

(CHIR) CHIRON CORP.

'V, Gale. P. Pizza M;

Rappuoli R,

WPI; 2000-318079/27.

99WO-US23573. 98US-0103794 99US-0132068

08-OCT-1999; 09-OCT-1998; 30-APR-1999;

20-APR-2000

; 0 2255 HHYWASYGKVKGNATKYNRYTKKSANKGHNATKYNRYTKKSANKGHHYWYTATNRYANAY 2196 11::| |:: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | 377 cttcctgttatgacagagcttgtgaactttaactgggactggggcaaagtcaatcccacc 436 437 tttatacaatgaattgctgaagaggccttttaaaaacttggagtgtgcattgtttatggaa 496 0; Gaps DB 20; Length 2274; Indels 80; Query Match 6.6%; Score 33.8; DB Best Local Similarity 15.5%; Pred. No. 0.44; Matches 30; Conservative 84; Mismatches : |: |: |: |: 2075 NDTYCTYTATHTDK 2062 497 gggctttcctattg 510 g g δ q ò 요 à ò

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0; Mismatches
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Query Match
Best Local Similarity 51.00
The 73; Conservative
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                                                                                                       A81473 standard; DNA; 92934 BP.
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04 - DEC - 2000

A81473;

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RESULT A81473

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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. A81453 to A82414 represent proteins from Neisseria genomic sequences. A81453 to A812414 represent corresponding by Neisseria meningitidis genomic DNA sequences and their corresponding proteins; A81254 to A81259 and A81304 to A81321 corresponding proteins; A81254 to A81259 and A81304 to A81321 corresponding proteins; A81254 to A81259 and A81304 to A81321 corresponding proteins; A81254 to A81259 and A81304 to A81321 corresponding proteins; A81254 to A81259 and A81304 to A81321 corresponding their corresponding proteins; A81452 represent Neisseria meningitidis DNA sequences; and A81322 to A81452 represent Neisseria meningitidis MenB composition. The nucleic acid sequences, protein sequences, and antibodies against them, can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified correspondences from the bacterium will also facilitate production of sequences from the bacterium will also facilitate production of correspondences from the bacterium will also facilitate production of cological probes, particularly organism specific probes. Attempts to antigen tolerance Multivalent vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have failed mainly due to antigen tolerance may provide an opportunity to identify expected or surface sequences may provide an opportunity to identify expected or surface exposed proteins that may be present expected or surface exposed proteins that may be presented or surface exposed proteins that may be presented.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune system and which are not antigenically variable or at least more conserved than other more variable regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
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Neisseria meningitidis B nucleotide sequence SEQ ID NO:1. F21544 standard; DNA; 349980 BP 13-MAR-2001 (first entry) F21544; RESULT F21544

Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;

Neisseria meningitidis

WO200066791-A1

09-NOV-2000

08-MAR-2000; 2000WO-US05928

30-APR-1999; 99US-0132068. 08-OCT-1999; 99WO-US23573. 28-FEB-2000; 2000GB-0004695.

(CHIR) CHIRON CORP. (GENO-) INST GENOMIC RES.

Masignani V; Rappuoli R; Venter JC, Scarlato V, Peterson J, Tettelin H, Ratti G, Scarselli M, Pizza M, Hickey E, Galeotti C, Mora M, Frazer CM, Grandi G;

WPI; 2000-647603/62.

Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections -

Claim 7; Appendix A; 692pp; English.

The present invention describes the full length genome of Neisseria menigitidis B (NMB). The sequences in F21544 and F21607 to F21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by which overlap each other at the beginning and end of each sequence by F21607, the last 49980 bp of F21544 is repeated at the beginning of F21607, the last 49980 bp of F21507 are repeated at the beginning of F21608, and so on). F21545 to F21560 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisserial nucleic acids, proteins and/or treating or preventing infection due to Neisserial bacteria or as a diagnostic regent of the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used.

Sequence 349980 BP; 83241 A; 85091 C; 95206 G; 86442 T; 0 other;

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Gaps
6.3%; Score 32.2; DB 21; Length 349980;
51.8%; Pred. No. 21;
iive 0; Mismatches 68; Indels 0;
                                    73; Conservative
                   Best Local Similarity
 Query Match
                                    Matches
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. A81453 to A82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; A81260 to A81303 and B25620 to B25663 represent Neisseria DNA sequences and their corresponding proteins; A81254 to A81259 and A81304 to A81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and A81322 to A81452 represent Neisseria meningitidis MenB polynucieotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins could be components of vaccines against Meningococcus B; against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify
                                    13884 tttgtgcatacctgtggattgtttttcatgaagaatagtttttgtggacagtttgcttgt 13943
                                                                                                      Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelsseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                              417 ggggcaaagtcaatcccacctttatacaatgaattgctgaagaggccttttaaaacttgg 476
357 tttgtgaccatctgcccattcttcctgttatgacagagcttgtgaactttaactgggact 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
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Ratti G, Scarselli M,
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Galeotti C, Mora M,
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Rappuoli R, Pizza M;
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secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.
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                                                                                                                                   357 tttgtgaccatctgcccattcttcctgttatgacagagcttgtgaactttaactgggact 416
                                               Sequence 1437668 BP; 344338 A; 353206 C; 385074 G; 355045 T; 5 other;
                                                                                                            Gaps
                                                                                   DB 21; Length 1437668;
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                                                                                                           68; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 67438
                                                                                  Query Match 6.3%; Score 32.2; DB Best Local Similarity 51.8%; Pred. No. 43; Matches 73; Conservative 0; Mismatches
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C51145 standard; DNA; 5520 BP
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09-MAR-1999

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990S-0146389.
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990S-0147204.
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99US-0153070.
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99US-0154018.
99US-0154039.
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990S-0155486.
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990S-0156596.
99US-0157117.
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990S-0158029.
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990S-0158369.
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99US-0151066.
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11-AuG-1999

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113-AuG-1999

113-AuG-1999
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1-OCT-1999;
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06-OCT-1999;
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                                                                                                                                                                                3739 GCACATAAGATGAAAAGAAAAGGTGAGGTCGCTCGTTGTCTAATGCCCCGTTCTGGT 3680
                                                                                                                                                      67 gtacacagcatgataaaagacaatgggacggggtcacagtggctcccgtccctttcaggg 126
                                                                                                                                  Gaps
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                                                                                                      Length 5520;
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                                                                                                                                                                                                           127 gtatggagacgagctgtagagagatgtctccagggagttttcattaatca 176
                                                                                                                                 Indels
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JM, Janat F, Lafleur DW, Ni J;
Shi Y, Young P, Yu G;
                                                                                                    DB 21;
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                                                                                                      6.1%; Score 31.6; D; 55.5%; Pred. No. 3.9; 1ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                 X37475 standard; cDNA; 1222 BP.
             990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
99US-0161993.
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97US-0060836.
97US-0060837.
97US-0060839.
97US-0060843.
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97US-0060874
 99US-0161359
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P-PSDB; X07876.
                                                                                                                  Best_Local Similarity
Matches 61; Conserv
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
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                                                                                                       Query Match
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This invention describes novel isolated human genes and the secreted

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Specific uses are described for each of the 101 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, prostate disease, skeletal or cradic muscle disorders, pulmonary disorders, transplant rejection, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseastive/endocrine disorders, infections and AIDS. The human secreted proteins of the invention are represented in X37451-X37552.
                             preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides.
proteins they encode. The products of the invention are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1222 BP; 402 A; 207 C; 243 G; 367 T; 3 other;
$$$$$$$$$$$$$$$$$$$$$$$$
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0 Length 1222; Indels DB 20; 6.0%; Score 30.8; DI 50.7%; Pred. No. 3.3; ative 0; Mismatches Local Similarity 50.7 tes 74; Conservative Query Match Best Local S: Matches 74

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agtitticatiaaicagcaatitagicagaicigigcaicciaigcittacaagaaaigic 221 222 agccatcattaataagggatctattggatactgttcttccacatctttacaatgaaacaa 281 222 agtgggcctgagatcatcagatggaggttcatcgggtttcaatgtcccgtatccttttgt 281 282 aagttagaaaggagcttataagagaggtagaaatgggtccatttaaacatacggttgatg 341 162 q à a

282 aagaccttgaagttggcaacgcagga 307 ò g

342 atggtctggatattagaaaggcagca 367

C76389 standard; cDNA; 5612 BP 08-FEB-2001 (first entry) C76389; RESULT 10 C76389

Human ORFX ORF1944 polynucleotide sequence SEQ ID NO:3887.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autofimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss

Homo sapiens

WO200058473-A2.

05-0CT-2000

31-MAR-2000; 2000WO-US08621.

99US-0127607. 31-MAR-1999;

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represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antichastic; antichastic; inmunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antichabetic; hypotensive; cardiant; thrombolytic; osteopatic; antichabetic; hypotensive; cardiant; thrombolytic; antichabetic; antichabetic; hypotensive; cardiant; thrombolytical; antithabetic; noredisposition to, or preventing or treating pathological conditions associated with an ORRY-associated disorder. The nucleic acids can be used to express ORRY proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglolability anticining anticining cartilage anaemia, burns, walling decoming cartilage anaemia, burns, anticininamia ant
                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 3033-3036; 5507pp; English.
                                 05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
99US-0127636
                                                                                                                                                                                                                    Shimkets RA, Leach M;
                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                       WPI; 2000-602362/57.
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02-APR-1999;
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Gaps Length 5612; 6.0%; Score 30.8; DB 21; 50.7%; Pred. No. 7.3; 0; Mismatches 74; Conservative Best Local Similarity Query Match Matches

Sequence 5612 BP; 1716 A; 985 C; 1121 G; 1788 T; 2 other;

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3158 agccatcattaataagggatctattggatactgttcttccacatctttacaatgaaacaa 3217 162 agtitticattaatcagcaatttagtcagatctgtgcatcctatgctttacaagaaatgtc 221 δò

222 agtgggcctgagatcatcagatggaggttcatcgggtttcaatgtcccgtatccttttgt 281 g ò

282 aagaccttgaagttggcaacgcagga 307 ò 3278 atggtctggatattagaaaggcagca 3303

RESULT 11 V31227

ВÞ V31227 standard; DNA; 314

V31227;

(first entry) 01-OCT-1998

E. coli J96 pathogenicity island contig #41.

PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.

Escherichia coli.

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99GB-0000710.
99GB-0000711.
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17-DEC-1998;
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28-JAN-1999;
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                                                                                                                                                                                                                                                           This sequence represents a E. coli strain J96 contig containing pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIs are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from PAI IV and PAI V. PAI IV is located at approximately 64 min (near phev) approximately 94 min (at phex) on the E. coli chromosome and is greater than 170 kb. PAI V is located at approximately 94 min (at phex) on the E. coli chromosome and is approximately 160 kb in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in kits to a protective immune response in an animal to the uropathogenic E. coli strain J96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 aacatcagagcagtcttctcgcttagaaaaagctttattaggttttacaaacacaatgta 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 aagtcaatcccacctttatacaatgaattgctgaagaggccttttaaaacttggagtgtg 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 accatctgcccattcttcctgttatgacagagcttgtgaactttaactgggactggggca 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virulence protein; tatA; tatB; tatC; tatE; mdoG; creC; recG; yggN; eckl; iroD; iroC; iroE; mtd2; ms1; vaccine; infection; Gram negative bacterium; ss.
                                                                                                                                                                                          New isolated uropathogenic E. coli nucleotide sequences - used to
                                                                                                                                                                                                     develop products for the detection of pathogenic {\tt E}. coli and to elicit an immune response to pathogenic {\tt E}. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 314 BP; 105 A; 56 C; 60 G; 92 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding Escherichia coli virulence proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%; Score 30.6; D
Best Local Similarity 52.8%; Pred. No. 1.9;
Matches 66; Conservative 0; Mismatches
                                                                                                                                                                                                                                       Claim 21; Page 139-140; 250pp; English.
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                                                                                                                                            Welch RA;
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                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                              97WO-US21347
                                                                                  96US-0031626
                                                                     97US-0061953
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                                                                                                                    UNIV WISCONSIN
                                                                                                                                           Choi GH, Dillon PJ,
                                                                                                                                                                  WPI; 1998-312461/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cattg 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cattg 208
WO9822575-A2
                                              21-NOV-1997;
                                                                     14-OCT-1997;
                                                                                  22-NOV-1996;
                        28-MAY-1998
                                                                                                                    (DXMI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A15186;
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                                                                                                                                                The present sequence encodes Escherichia coli virulence proteins
The specification describes virulence proteins which are encoded
by an operon including tath, tath, tatc, tatk, mdog, creC, recg, yggN,
eckl, iroD, iroC, iroE, mtd2 or msl-16 genes obtained from Escherichia
coli KI. The virulence proteins and polynucleotides, and their vaccines
are useful for screening potential drugs, for the detection of virulence,
and for treating or preventing conditions associated with infection by
                                                                                  Peptide encoded by an operon including genes from Escherichia coli for screening potential drugs, detecting virulence and treating conditions associated with infection by a Gram negative bacterium -
                                                                                                                                                                                                                                                                                                                                                                              5585 aacatcagagcagtcttctcgcttagaaaagctttattaggttttacaaacacaatgta 5644
                                                                                                                                                                                                                                                                                                                        363 accatctgcccattcttcctgttatgacagagcttgtgaactttaactgggactggggca 422
                                                                                                                                                                                                                                                                                                                                                                 482
                                                                                                                                                                                                                                                                                                     Gaps
                     Shea JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid for use in diagnostic and analytical methods
                                                                                                                                                                                                                                                                                                                                                                 423 aagtcaatcccacctttatacaatgaattgctgaagaggccttttaaaaacttggagtgtg
                                                                                                                                                                                                                                                                               5.9%; Score 30.6; DB 21; Length 11165; 52.8%; Pred. No. 12;
                                                             P-PSDB; Y93237, Y93238, Y93239, Y93240, Y93241, Y93242, Y93243.
                                                                                                                                                                                                                                               Sequence 11165 BP; 3592 A; 2087 C; 2458 G; 3028 T; 0 other;
                     Holden DW,
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                           Gram negative bacterium particularly Escherichia coli.
                                                                                                                                                                                                                                                                                                   59;
                    Everest PH, Dougan G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis R;
                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                             Disclosure; Page 83-101; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia pneumoniae genome DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C81914 standard; DNA; 273254 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US26923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0108279
99US-0128606
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(MICR-) MICROSCIENCE LTD.
                                                                                                                                                                                                                                                                                                    66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitchell W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                     Clarke EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae.
                                                   2000-376550/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-376516/32
                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              5705 cattg 5709
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08-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2000
                               Feldman RG
                     Crooke HR,
                                                                                                                                                                                                                                                                               Query Match
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This invention describes a novel nucleic acid (NI) encoding a Chlamydia pneumoniae protein (PI), given in the specification. The isolated nucleic acid is useful for diagnostic and analytical methods, such as, card is useful for diagnostic and analytical methods, such as, chybridization-based assays or amplification-based assays. The protein may be used for diagnostic purposes, for their enzymatic or structural activity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizes under stringent conditions to NI; (3) an expression cassette comprising fragment of NI; (2) an isolated nucleic acid (N2) that hybridizes under stringent conditions to NI; (3) an expression of a transcriptional initiation region functional in an expression host, and a transcriptional termination region functional in an expression host, and a cassette of (3) as part of an extrachromosomal element or integrated into the genome of a host cell as a result of induction of the expression cassette into the host cell, and the cellular progeny of the host cell; (5) a method for producing a PI comprising growing a cell of (4) where the protein is expressed and isolating the protein free of other proteins; (6) a purified polypeptide composition comprising at least 50 expression and a part of the protein free of other proteins; (6) a purified polypeptide composition comprising at least 50 expression and isolating antibody binding specifically to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; creebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungloide; neoplasm; opthalmalogical; autoimmune disease; rheumatoid arthritis; angiogenesis; phyperproliferative disorder; cardiovascular disorder; infection; crebrovascular disorder; nervous system disorder; infection; wound healing; chemotaxis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31730 actgretttacgatgaagacagetttteactettgetattettggttttgttggtcttt 31789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 gtctccagggagttttcattaatcagcaatttagtcagatctgtgcatcctatgctttac 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 aagaaatgtcagtgggcctgagatcatcagatggaggttcatcgggtttcaatgtcccgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 atccttttgtaagaccttgaagttggcaacgcaggaaaacaggaactccaccctggtgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 273254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 gtgaattgcagagctgttgtgttggtttgtgaccatctgcccattcttc 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
encodes genomic sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein gene 31 SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30.6; 1
Pred. No. 64;
                                                                                   Claim 2; Page 128-320; 320pp; English.
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Matches 105;
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C74253
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98DE-1017948 98DE-1017948

17-APR-1998; 17-APR-1998; 21-OCT-1999

DE19817948-A1.

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The polynucleotide sequences given in C74223-C74279 encode the human secreted proteins represented in B39179-B39226. Sequences B39227-B39308 are alternative proteins encoded by the genes, and also protein sequences with which they share homology. The proteins have activities based on the tissues and cells in which they are expressed Examples of activities ancinclude: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antiarthriticmal; virucide; fungicide; and opthalmalogical. The human secreted proteins, polynucleotides, antiartagonists and agonists of the invention may be useful in the treatment, prevention, and/or diagnosis of various disease, disorders and conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as autoimmune diseases e.g. rheumatoid arthritis, they preproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. carbral ischaemia, angiogenesis, nervous system disorders e.g. carbral ischaemia, infections caused by bacteria, viruses and fungi and cular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to regenerate tissues, maintain organs before transplantation, in chemotaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and as a food additive or preservative e.g. to increase storage capabilities. Sequences C74214-C74222 and B39178 are used during the isolation and characterisation of the genes of the invention.
                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition \,
                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 357-358; 434pp; English.
                                                                                                                                                 Komatsoulis G;
                                                                                           (HUMA-) HUMAN GENOME SCI INC
                    99US-0125362.
99US-0169980.
                                                                                                                                           Ruben SM,
                                                                                                                                                                                            WPI; 2000-579483/54
                                                                                                                                                                                                                     P-PSDB; B39209
                    19-MAR-1999;
                                             10-DEC-1999;
                                                                                                                                         Rosen GA,
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Sequence 3161 BP; 1025 A; 485 C; 603 G; 1048 T; 0 other;

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                                                                                                                     1716 ccatttgtgaaatcatcaaagagatgttaatcctgctttagcattgatgcaaagttaaaa 1775
                                                                                                                                                                                                        1776 taactgacattaaaaaaaatcatttgggaagctttattgaatattgagataagggttaa 1835
                                                                               372 ccattcttcctgttatgacagagcttgtgaactttaactgggactggggcaaagtcaatc 431
                                                                                                                                                              432 ccacctttatacaatgaattgctgaagaggccttttaaaaacttggagtgtgcattgttta 491
                                            Gaps
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Ouery Match 5.9%; Score 30.4; DB 21; Length 3161; Best Local Similarity 50.7%; Pred. No. 7.4;
                                            Indels
                                          71;
                                        0; Mismatches
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                                        73; Conservative
                                          Matches
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0; Gaps

40;

0; Mismatches

Local Similarity 57.4 ies 54; Conservative

Query Match Best Loca Matches ŏ

1 tttaaatgtgctgtctttagaagccactgcctcagcttctgcagctcagataccaaagga 60

5.8%; Score 30; DB 20; Length 692; 57.4%; Pred. No. 4.5;

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Search completed: June 21, 2001, 18:06:24
                             Job time: 13792 sec
                                                                                                                                                                                                                                                                                                                                                                                                         Endometrium; human; tumour; cancer; anticancer; cytostatic; EST:
                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment; uterine; gene therapy; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                           Human endometrium tumour cDNA derived EST 32.
                                                                                                                                                242012 standard; cDNA; 692 BP
                                                                                                                                                                                                                                                                             31-JAN-2000 (first entry)
                                                                                                                                                                                                                  242012;
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RESULT 242012 Homo sapiens

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that are highly expressed in utarian incited (CDM) sequences (A), and anticancer and cytostatic activity. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs (expressed expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. 241981-242121 represent EST fragments derived from a human endometrium tumour CDM, library which encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel human nucleic acid (cDNA) sequences (A),
                                                                                                                                                                                                                                      Dahl E;
                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents
                                                                                                                                                                                                                                    Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 692 BP; 146 A; 189 C; 197 G; 160 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein sequences represented in Y59941-Y60328
                                                                                                                                                                                          (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                      Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 190; 444pp; German.
                                                                                                                                                                                                                                                                                              P-PSDB; Y60034, Y60035, Y60036.
                                                                                                                                                                                                                                    Rosenthal A, Specht T,
                                                                                                                                                                                                                                                                            WPI: 1999-591957/5
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 21, 2001, 18:20:53 ; Search time 150.46 Seconds (without alignments) 634.116 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-445-201-1_COPY_10094_10608 515 1 tttaaatgtgctgtctttag......agggctttcctattggatcc 515

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

635060 Total number of hits satisfying chosen parameters:

317530 seqs, 92630169 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*

(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

(cgn2_6/ptodata/2/ina/5B_COMB.seq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/pCTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/pCTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/pcTus_company)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	5-16 Sequence 16, App.		64 Sequence 6	7 Sequence 27,	7 Sequence 27,	-27 Sequence 27,	-27	-88 Sequence 88,	Sequence 7, 1	Sequence 1,	-19 Sequence 19,	4 Sequence 4,		-1 Sequence 1,	3 Sequence 3,	Sequence 4,	1 Sequence 11,	1 Sequence 11,	Sequence 1, P	l Sequence 1,	l Sequence 1,	-1 Sequence 1,	Sequence 2,	Sequence 2,	Sequence 22,	2 Sequence 22,	Segmenter 22
SUMMARIES	QI	US-09-128-15	5248670-4	US-09-032-365A	US-08-434-255-2	US-08-459-967	US-08-460-327-2	US-08-459-871	US-09-276-531	US-09-130-242-	US-09-130-242-	US-08-387-942C	US-08-883-534	US-09-204-764-	US-08-387-942	US-08-985-950-3	US-08-510-790-4	US-09-234-163-1	US-08-901-379-1	US-08-254-358-1	US-08-475-391	US-08-709-609-	PCT-US95-07178	US-08-331-384-	US-08-836-087-2	US-08-480-784-2	US-08-483-553-2	TS-08-487-003-
	DB DB	4	9	4	, -1	 1	-	Н	7	4	4	7	7	m	7	4	~1	3	4	Н	~	7	Ŋ	7	7	П	П	7
	Length DB	LC)	3688	2088	2017	2017	2017	2017	410	751	3773	1143	2369	2369	12588	376	349	2236	2236	4680	4680	4680	4680	4910	4910	710	710	710
đ	Query	5.7	5.7	5.6	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3
	Score	29.6	29.5	28.8	28.4	28.4	28.4	28.4	28.2	28.5	28.2	28	28	28	28	27.8	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.2	27.2	27.2
	ult No.	-	7	٣	4	2	9	7	ထ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27
	Result No.	ပ	O		O	υ	υ	υ				ပ	υ	o	U	U		υ	υ					υ	υ	υ	υ	O

Sequence 22, Appl Sequence 2, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 2, Appl Sequence 3, Appl Sequence 6, Appl Sequence 8, Appl Sequence 8, Appl Sequence 9, Ap	RELATED PROTEIN FAMILY	4; Length 152331; 64; Indels 0; Gaps 0; catcctatgctttacaagaaa 217 [
710 1 US-08-483-554B-22 710 1 US-08-488-011B-22 710 5 PCT US95-10202-22 710 5 PCT US95-10203-22 710 5 PCT US95-10203-22 710 5 PCT US95-10203-22 710 5 PCT US95-10203-22 710 5 PCT US95-10203-22 5656 1 US-08-825-886-1 5656 1 US-08-825-886-1 5707 1 US-08-425-061-1 5707 1 US-08-825-886-1 5707 1 US-08-825-886-1 5709 1 US-08-825-866-1 5709 1 US-08-825-061-7 5709 1 US-08-425-061-7 5709 1 US-08-425-061-7 5709 1 US-08-425-061-7 5709 1 US-08-425-061-7 5709 1 US-08-425-061-7	ALIGNMENTS ion US/09128155 NOVEL MOLECULES OF TANGO-77 AND USES THEREOF 1998-08-03 NUMBER: US/091,650 1998-07-02 NUMBER: US 60/091,650 1998-07-02 NUMBER: US 60/054,646 1997-08-04 i: 18 ir Windows Version 3.0 ure in = A,T,C or G	5.7%; Score 29.6; DB 1.5%; Pred. No. 41; ve 0; Mismatches caqcaatttagtcagatctgtg.
0 28 0 29 0 31 0 31	RESULT 1 US-09-128-155-16/C Sequence 16, Application US/09128155 Patent No. 6117654 GENERAL INCORMATION: APPLICANT: Pan, Yang TITLE OF INVENTION: NOVEL MOLECULES (TILE OF INVENTION: NOVEL MOLECULES (TILE OF INVENTION: NOVEL MOLECULES (TILE NETENT FILLING DATE: 1998-08-03) EARLIER PELLING DATE: 1998-07-02 EARLIER PILING DATE: 1998-07-02 EARLIER PILING DATE: 1997-08-04 NUMBER OF SEQ ID NOS: 18 SCOTWARE: FASTESEQ for Windows Version SEQ ID NO 16 LENGTH: 152331 TYPE: DNA ORGANISM: HOMO SAPIENS FRATURE: COCATION: (152331) COCATION: (152331) COCHER INFORMATION: n = A,T,C Or G	Ouery Match Best Local Similarity 5 Matches 68; Conservati Qy 158 agggagtttcattaat

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Query Match
Best Local Similarity
Matches 69; Conserv
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US-08-434-255-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: N
STATE:
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                                                                                                                                                                                                                                                                                                   340 cagagotgttgtgttggtttgtgaccatctgcccattcttcctgttatgacagagottgt 399
                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                    Score 29.2; DB 6; Length 3688;
Pred. No. 7.1;
0; Mismatches 38; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: No. 6114502th, Michael
APPLICANT: Nishina, Patsy
APPLICANT: Naggart, Juergen
APPLICANT: Naggart, Juergen
APPLICANT: No. 6114502en-Trauth, Konrad
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
TITLE OF INVENTION: NEUROSENSORY DEFECTS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR ;INHIBITING HERRESVIRUS ; NUMBER OF SEQUENCES: 15 ; CURRENY APPLICATION DATA: APPLICATION NUMBER: US/07/485,297 ; FILING DATE: 26-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FEASTERD for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         400 gaactttaactgggactggggcaaagtcaa 429
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; Sequence 64, Application US/09032365A
; Patent No. 6114502
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                     Query Match 5.7%;
Best Local Similarity 57.8%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 2008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650 327-3231
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MOLECULE TYPE: CDNA
US-09-032-365A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                  , LENGTH: 3688
5248670-4
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                                                                                                          SEQ ID NO:4:
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                                                                                                                                                           67 gtacacagcatgataaaagacaatgggacggggtcacagtggctcccgtccctttcaggg 126
                                                                                                         355 ggtttgtgaccatctgcccattcttcctgttatgacagagcttgtgaactttaactggga 414
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5.6%; Score 28.8; DB 4; Length 2088; 50.7%; Pred. No. 7.1; tive 0; Mismatches 67; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28.4; DB 1; Length 2017; Pred. No. 9.5;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sloma, Alan P.

APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Dambmann, Claus
APPLICANT: Asalyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. cf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/434,255 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 27, Application US/08434255; Patent No. 5621089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Agris Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFRENCE/DOCKET NUMBER: 3764
TELEPONMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
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212-878-9655
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nucleic acid
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Best Local Similarity 54.99
Matches 56; Conservative
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                                         Conservative
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10174-6401
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US-08-434-255-27/c
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                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,967
FILING DATE: 02-UNN-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: US/08/434,255
FILING DATE: 03-MAY-1995
ATONEY/AGENT INFORMATION:
NAME: Agris Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
RECISTRATION NUMBER: 34,086
RECISTRATION NUMBER: 34,086
RECISTRATION NUMBER: 31.086
RELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
INFORMATION FOR SED. ID NO: 27:
CONTINUED FOR SED. ID NO: 27:
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APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESSPONDENCE ADDRESS:
ADDRESSEE: No. 56228410 No. 5622841dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08.460.327-27/c

Sequence 27, Application US/08460327

Patent No. 5622850

GENERAL INFORMATION:

APPLICANT: Sloma, Alan P.

APPLICANT: Outtrup, Helle

APPLICANT: Dambmann, Claus

APPLICANT: Asslyng, Dorrit

TITLE OF INVENTION: ALRALINE PROTEASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
                       Sequence 27, Application US/08459967
Patent No. 5622841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2017 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                   STREET: 405 LexinCITY: New YorkSTATE: New YorkCOUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POPOLOGY: linear
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US-08-459-967-27/C
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No. 56503260 No. 5650326disk of No. 5650326th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 GCTTTGTTCAGAGCAGAACCTTGTGCCTTTTTGGATACACCATCTTTGAATTGACGATGA 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 ctggggcaaagtcaatcccacctttatacaatgaattgctga 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,327
FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 405 Lexington Avenue, 64th Floor CITY: New York STRATE: New York STRATE: New York ZIP: 10174-6401 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/08459871
Patent No. 5650326
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambann, Claus
APPLICANT: Dambann, Claus
APPLICANT: Dambann, Claus
APPLICANT: ABASIYNG, DORTIT
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56503260 No. 5650326dis
                                                                                                                                                                                                                                                                                                                                                                                             NAME: AGTIS Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
                                                                                                                                                                                                                APPLICATION NUMBER: US/08/460,327
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/459,871
FILING DATE: 02-JUN-1995
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 2017 base pairs
                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
               COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-459-871-27/C
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US-08-460-327-27
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INFORMATION FOR SEQ ID NO:
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US-09-130-242-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Tue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 ggittgigaccatctgcccattcttcctgttatgacagagcttgtgaactttaactggga 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 GCTTTGTTCAGAGCAGGACCTTGTGCCTTTTTGGATACACCATCTTTGAATTGACGATGA 364
                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM P. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
RILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PA-0008 US 
FELECOMMUNICATION INFORMATION: 
TELEPHONE: (650) 855-0555 
TELERAX: (650) 845-4166
APPLICATION NUMBER: US 08/434,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 88, Application US/09276531
Patent No. 6183968
             FILING DATE: 03-MAY-1995
ATORNEY/AGENT INFORMATION:
NAME: AGTIS Dr., CHEYL H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764,
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHRARCTERISTICS:
LENGTH: 2017 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.5%
Best Local Similarity 54.9%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-459-871-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
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GENERAL INFORMATION:
APPLICANT: Gianturco, S.H.
APPLICANT: Gianturco, S.H.
APPLICANT: Bradley, W.A.
TITLE OF INVENTION: DA Encoding Human Monocyte-Macrophage Applipoprotein
TITLE OF INVENTION: B Receptor Gene and Protein
TITLE OF INVENTION: B Receptor Gene and Protein
CURRENT APPLICATION NUMBER: US/09/130,242B
CURRENT FILING DAFE: 1998-08-06
SURRENT FILING DAFE: 1998-08-06
SOFTWARE: MS WORD, Macintosh OS 8.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gianturco, S.H.
APPLICANT: Bradley, W.A.
TITLE OF INVENTION: DN Encoding Human Monocyte-Macrophage Applipoprotein
TITLE OF INVENTION: B Receptor Gene and Protein
FILE REFERENCE: D5880
CURRENT APPLICATION NUMBER: U5/09/130, 242B
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: MS WORD, Macintosh OS 8.5
                                                                                                                                                                                                                                                                                                                                                                                                                               71 AATCTTGCTGTGCCAAGAATAAAGTCAACTTCATATTTATATAGTTATATTATCCGGAGA 130
                                                                                                                                                                                                                                                                                                                                                                                  402 actttaactgggactggggcaaagtcaatcccacctttatacaatgaattgctgaagagg 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.5%; Score 28.2; DB 4; Length 410;
53.1%; Pred. No. 4.5;
Live 0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 acggggtcacagtggctcccgtccctttcagggggtatggagacga 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28.2; DB
Pred. No. 6.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09130242B Patent No. 6194558
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54,3%;
                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 53.1%
Matches 60, Conservative
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Best Local Similarity 54.38
Matches 57; Conservative
                          410 base pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                 TOPOLOGY: linear
| IMMEDIATE SOURCE:
| LIBRARY: PROSTUT08
| CLONE: 1651564
| US-09-276-531-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapien
US-09-130-242-7
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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; CLONE: 1221143
US-08-883-534-4
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic a STRANDEDNESS: 6 TOPOLOGY: linea IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
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                                                                                                                               Query Match 5.5%; Score 28.2; DB 4; Length 3773; Best Local Similarity 54.3%; Pred. No. 16; Matches 57; Conservative 0; Mismatches 48; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ERTESYAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  345 ctggggagatggcagctcccatgggtcccaagcagagaggcagga 389
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ZIP: 22042

COMPUTER: PLORPY disk
MEDIUM TYPE: Florpy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FTLING DATE: 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O.BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                US-08-387-942C-19/c
; Sequence 19, Application US/08387942C
; Patent No. 5939289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REPERENCE/POCKET NUMBER: 1809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic) US-08-387-942C-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1143 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703-205-8050
                                 ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-130-242-1
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SEQ ID NO 1
LENGTH: 3773
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363 accatctgcccattcttcctgttatgacagagcttgtgaactttaactgggactggggca 422
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OPERATING SYSTEM: DOS
SOFTWARR: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,534
                                                                                                                                                                                                              APPLICANT: Bandman, olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0332 US
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Sequence 4, Application US/09204764

Patent No. 6025464

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                            US-08-883-534-4/c
; Sequence 4, Application US/08883534
; Patent No. 5846777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.4%;
Best Local Similarity 58.3%;
Matches 49; Conservative
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COUNTRY:
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Patent No. 593928
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SAJAK-BRAEK, GUDMUND
APPLICANT: SAJAK-BRAEK, GUDMUND
APPLICANT: SAJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O.BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/204,764
FILING DATE:
CLASSIFICATION S:
PRIOR APPLICATION NUMBER: 08/883,534
FILING DATE:
ATTORNEY,AGENT INPORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: 36,749
APPLICANT: Lal, Preeti
APPLICANT: COTLEY, Neil C.
TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
WUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 aagtcaatcccacctttatacaat 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 58.38
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: NEUTGMT01
CLONE: 1221143
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                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 94304
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US-08-387-942C-1/c
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5694 GACCTGGCTGTCGTCGAAGGCCTGCAGCAGGACTTCCGGATAGGTGCCGTTCTGCGAATT 5635
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APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 2; Length 12588;
Pred. No. 36;
0; Mismatches 45; Indels
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                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 getgttgtgtttgttgtgaccatctgcccattcttcctg 383
                                                                                                                       APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Azotobacter vinelandii
STRAIN: E
                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-985-950-3/c
; Sequence 3, Application US/08985950
; Patent No. 6140076
                                                                                                                                                                                                                                                                                                       TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs
TYPE: nucleic acid
cTRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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Best Local Similarity 55.0%;
Matches 55; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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9973..12588
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2227..6438
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6702..9695
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: US/08/085,950
FILING DATE: US/08/085,950
PIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
ATTONNEY/ACENT INFORMATION:
FILING DATE: U6-DEC-1996
ATTONEY/ACENT INFORMATION:
FILING DATE: U6-DEC-1996
ATTONEY/ACENT INFORMATION:
FILING DATE: U6-DEC-1996
ATTONEY/ACENT INFORMATION:
REGISTRATION NUMBER: 34,090
REFRENCE/DOCKET NUMBER: 34,090
REFRENCE/DOCKET NUMBER: 2104
TELEPHONE: (650)496-1204
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 base pairs
TOPOLOGY: linear
MOLEGULE TYPE: CDNA
FEATURE:
MAME/KEY: CDS
NAME/KEY: CDS
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Search completed: June 21, 2001, 18:21:24 Job time: 17477 sec

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em_esthum28:*
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em_esthum14:*
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June 21, 2001, 15:33:59 ; Search time 4579.66 Seconds (without alignments) 1063.009 Million cell updates/sec
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    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                    10228115 seqs, 4726426750 residues
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Maximum Match 100%
Listing first 45 summaries
                                 OM nucleic - nucleic search, using sw model
                                                                                                              IDENTITY_NUC Gapox 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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em_gss_inv3:* em_gss_other:* em_gss_pln1:*

em_gss_vrt1:*
em_gss_vrt2:*
em_gss_vrt3:*
gb_gssl:*

gb_gss2:* gb_gss3:* gb_gss4:*

gb_gss5:*
gb_gss6:*
gb_gss7:*
gb_gss9:*
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9b_9ss12:*
9b_9ss13:*
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9b_9ss15:*
9b_9ss15:*

em_gss_rod3:* em_gss_rod4:* em_gss_rod5:*

em_gss_pln2:* em_gss_pro:* em_gss_rod1:* em_gss_rod2:*

gb_estill: gb_htc:* em_gss_fun:* em_gss_huml:* em_gss_humd:* em_gss_humd:*

gb_est110:*

em_gss_hum5:* em_gss_hum6:* em_gss_hum7:* em_gss_hum4:*

em_gss_hum8:* em_gss_hum9:* em_gss_inv1:* em_gss_inv2:*

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9b-est99:*
9b-est100:*
9b-est1100:*
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9b-est91:*
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em_estro22:*
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gb_est107:*
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gb_est90:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. em_gss_inv4:*
em_gss_rod6:*
em_gss_rod7:*
em_gss_rod8:*
gb_gss35:*
gb_gss36:*
gb_gss37:*

gb_gss30:* gb_gss31:* gb_gss32:* gb_gss33:*

gb_gss21:*
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gb_gss23:*
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gb_gss25:* gb_gss26:* gb_gss27:* gb_gss28:* gb_gss29:*

gb_gss18:*
gb_gss19:*
gb_gss20:*

Description	 007 1M011	440 20293 Ld	EST334	BG307433 fm15a04.y	BG456937 NF099G02P	BE505560 dc25d01.x	AQO34101 HS_Z1Z6_B BG457226 NF101a050	BF640846 NF058D111	BF642756 NF070F061	BG45/415 NF106A08P	AW689627 NF022E07S	BF637629 NF040D03P	AZ656206 1M0531B10	BF617491 HVSWEC001	BE324147 NF015A12P	BE317241 NF056C03L	AES 23 / 38 NF 00 / E08 P	AW776405 EST335470	AW683376 NF011D05L	BF638064 NF041C05P	BE123900 EST394091 BE005312 EST433810	AW981299 EST392452	BF006418 EST434916	BE249416 NF014H12L	AZB/DB69 ZMUL9UELI BF637320 NF074A01L	AW776060 EST335125	BF520706 EST458179	BE243340 NFU14DULL AW776945 EST336010	BG449793 NF053A03I	BF641416 NF061H061	AW / 09/1 EST350U30 BE318918 NF004H04T	AW775661 EST334726	BG449849 NF053G111	BF006087 EST434657	AW693996 NF071C09S		GSS 02-OCT-2000 library Mus musculus genomic			tebrata; Euteleostomi; Muridae; Murinae; Mus.	Duval, B., Hamil, C.,	reuersen,i., keiliy von Niederhausern,A.	
SUMMARIES	2 AZ364007 AA067448	7																																	AW693996	ALIGNMENTS	DNA blasmid UUGC1M	, DNA sequence. 07		Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae	rber, M., Beacorn, T., Du Mahmond M. Mooner F	Stokes, R., Tingey, A.,	
Length DB	24:	23/	12(631 150										14007 586 bp 110F03F Mouse 10kb F	GI:104777	· v	Metazoa; Ch utheria; Ro	to 586) yagi,A., Bal ongacte S	Rose, M., Rose, R., Wright, D., Weiss, R.	
% Query Match	 m		. 9	.8	ه. د	7.0	. 60	.8	œ. د		.8	9.	٥.	.4	.2 6	9,0	9.0	.5	91	7.0	. 7.	.2	9,0	7.0	9 9	2,0	4.9	. 7	.2	91	. 7	.2	91	2 0	9		12364007 IM0110F03F	AZ364007 AZ364007	GSS. house mouse. Mus musculus	Eukaryota; Metazoa; Mammalia; Eutheria;	1 (bases 1 to 586) Dunn,D., Aoyagi,A., Islam H. Longacte	D.W.	
Result No. Score	 37	, , ~	4 34	34	94	9 33	9 6	10 33	11 33	13 33	14 33	15 33	17 33	18 33	19 33	20 33	22 33	23 33	24 33	26 23	27 33	28 33	29	31 33	32 33	33 33	35 33	36 33	37 33	38 33	40 33	41 33	42 33	44 33	45 33		RESULT 1 AZ364007 LOCUS DEFINITION 1	ACCESSION P			AUTHORS D	, • 0	

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high modar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114) (pplART29072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA067448 409 bp mRNA EST 06-NOV-1997
26293 Lambda-PRLZ Arabidopsis thaliana cDNA clone 91F10T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                   1.586 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCIM0110F03" /clone="Lib="mouse 10kb plasmid UUGCIM library" /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 162; DB 242; Length 586;
Pred. No. 2.6e-39;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: F column: 03
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 586 Location/Qualiflers
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AA067448
AA067448.1 GI:1565781
EST.
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99.4%;
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Best Local Similarity 99.47
Matches 162; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 source
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AA067448/c
LOCUS
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Contact: Wing RA
Clemson University Genomics Institute
Clemson University
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AW775452.1 GI:7765265
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barrel medic.
Medicago truncatula
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Best Local Similarity 56.0%
Matches 70; Conservative
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AW775452/c
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                                                                                                                                                   1 (bases 1 to 409)
Newman,T., Gabrull,N.F.J., Green,P., Keegstra,K., Kende,H., McIntosh
L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
E. and Somerville,C.
                                                                                                                                                                                                                                 Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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Coryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 481)
Wing, R.A. and Dean, R.A.
Whoplished (1998)
                                                     Eukaryofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ866634 481 bp DNA GSS 03-NOV-1999 nbeb0028L19f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0028L19f, DNA sequence.
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Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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Pred. No. 1.3;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: 22313tcn@ibm.cl.msu.edu
Seg primer: T7 dye primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Thomas Newman
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Best Local Similarity 64.3%;
Matches 54; Conservative (
                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 517-353-0854
Fax: 517-353-9168
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/db_xxer= 'daxon.i4530''
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/clone="labol0281.9f"
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/tissue_type="Leaf"
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/lab_host="E. coii DH108"
/note="wector: pBACIndigo: Site_1: ECORI; Site_2: ECORI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly opulated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Barle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using ECORI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximaley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu):"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW775452 627 bp mRNA EST 07-SEP-2000 EST334517 DSIL Medicago truncatula cDNA clone pDSIL-1H24, mRNA
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100 Jordan Hall, Clemson, SC 29634, USA
                             Tel: 864 656 7288
FPA: 864 656 429
FPA: 864 656 429
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 36
High quality sequence stop: 412.
                                                                                                                                                                                                                                                                                                                                                                   1. .481
/organism="Oryza_sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Medicago truncatula
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Best Local Similarity 55.9%
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/lab_host="E. coli strain XLOLR"
/lab_host="E. coli strain XLOLR"
/note="Vector: paluescript SK-; Site_1: ECORI; Site_2:
/note="Vector: paluescript SK-; Site_1: ECORI; Site_2:
XhoI; CDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifoli: The CDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Giapaex III Gold packaging
extracts. Plasmids containing CDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells. Note: EST may
be of fungal origin."
                                                                                                                                                                                                                                                        Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
TTE: 612 625 1243
Fax: 651 649 5058
                                                                                      Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Peng, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.

ESTs from leaves of Medicago truncatula after inoculation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG307433 658 bp mRNA EST 22-FEB-2001
fml5a04.yl Zebrafish adult retina CDNA Danio rerio CDNA clone
4146318 5' similar to TR:P79895 P79895 TRANSDUCIN ALPHA SUBGNIT.;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 GGGAAGCIGAACIGIGACIGGGGGGTAGICAAICCCAICITICICCICAAATIIGACAGA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 gigaacittaacigggaciggggcaaagtcaatcccaccittatacaaigaatigcigaa 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="leaves infected with Colletotrichum trifolii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 34.8; DB 120; Length 627; 58.8%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 gaggccttttaaaaacttggagtgtgcattgtttatggaaggg 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 545 GCCGTCTGATGAAACCTCAAAGGGTCCTTCAATCTCGTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                       Minnesota sequence name:M258785e
TIGR sequence name:MTPAD48TK
MORE information is available at.
http://chrysie.tamu.edu/medicago
                                                                                                                                                                                                                                                                                                                                                                              Email: debbys@puccini.crl.umn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="pDSIL-1H24"
/clone_lib="DSIL"
                                                                                                                                                                                                                                         Contact: Deborah A. Samac
                                                                                                                                                                                      Colletotrichum trifolii
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG307433.1 GI:13104951
                                                                       (bases 1 to 627)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BG307433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Matches
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BG307433/c
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                                                                       REFERENCE
                                                                                             AUTHORS
                                                                                                                                                                                                              JOURNAL
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                TITLE
                                                                                                                                                                                                                                    COMMENT
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.

(Lases 1 to 658)

(Lases 1 to 658)

(Lark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. Washu Zebrafish EST Project 1998

Unpublished (1998)

Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library constructed by: Susan E. Brockerhoff DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagooliophyta; eudicotyledons; core eudicots; Sosidae; eucosida I; Fabales; Fabaceae; Papilionoideae; Medicago. I (bases I to 670)
Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores Far, Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Unpublished (2000)
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//dev_stage="1-2 years"
//lab_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')"
//note="Vector: Lambda ZAP II (pBluescript SK-); Site_1:
EcoRI; Site_2: Sall; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
a 149 c 158 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFO99G02PLIF1018 Phosphate starved leaf Medicago truncatula cDNA clone NF099G02PL 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 ccgtatccttttgtaagaccttgaagttggcaacgcaggaaaacaggaactccaccctgg 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647 CCTTAAGGTTTTCTTTGATGATAATGTCTGTCACGGCGTTAAACACAATCTCGACGTTCT 588
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Zebrafish adult retina cDNA"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 34.8; DE 55.9%; Pred. No. 8.5; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .658
/organism="Danio rerio"
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High quality sequence stop: 417.
Location/Qualifiers
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/db_xref="taxon:7955"
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COMMENT

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1 (bases 1 to 436)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ694161 436 bp DNA GSS 06-JUL-1999
HS_2126_B2_D11_T7C_CIT_Approved Human Genomic Sperm Library D Homo
spanens genomic clone plate=2126 Col=22 Row-H, DNA sequence.
AQ694161. GI:5384409
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High Throughput Sequencing Center University of Mashington University of Mashington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Eax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 2126 row: H column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CIT Approved Human Genomic Sperm Library D"
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E-Coli DH10B"
114 c 85 g 77 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 atggagacgagctgtagagagatgtctccagggagttttcattaatcagcaatttagtca 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 136; Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Indels
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/clone="Plate=2126 Col=22 Row=H"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%; Score 33.8; D
Best Local Similarity 50.0%; Pred. No. 16;
Matches 83; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Score 34.2; D
Pred. No. 12;
0; Mismatches
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Best Local Similarity 58.3%;
Matches 60; Conservative
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AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
/db_xref="taxon:3880"
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/clone="NR0996020L"
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/clone="logogo."
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/closue_type="logogo."
/dev_stage="trifoliate"
/dev_st
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Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (CLNL)
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primaer: -400P from Glabco.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

        BE505560
        411 bp
        mRNA
        EST
        06-AUG-2000

        dc25d01.x1
        NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:3398113

        x1
        mRNA sequence.

        BE505560
        GI:9709019

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1 (bases 1 to 411)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 gtgaactttaactgggactggggcaaagtcaatcccacctttatacaatgaattgctgaa 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%; Score 34.8; DB 153; Length 670; 58.8%; Pred. No. 8.6; Live 0; Mismatches 42; Indels 0;
                                              Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: G70 Std Error: 0.00
Plate: 099 row: G column: 02
Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                         Contact: Harrison MJ
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Matches 60; Conserv
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Query Match

DEFINITION

BE505560

RESULT

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ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BASE COUNT ORIGIN

FEATURES

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source

FEATURES

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1 (bases 1 to 654)
Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,
J.H., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
                                                                                                                                                                                                              Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Rosidae, eurosids I; Fabales; Fabaceae, Papilionoideae, Medicago.
                                                  BF640846 654 bp mRNA EST 19-DEC-2000 NF058D11IN1F1093 Insect herbivory Medicago truncatula cDNA clone NF058D11IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 Plant Science Bullding, Fayetteville, AR 72701, USA Tel: 501 575 5191
Fax: 501 575 7601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: kkorth@comp.uark.edu
Insert Length: 654 Std Error: 0.00
Plate: 058 row: D column: 11
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
                                                                                                                                           BF640846,1 GI:11905004
                                                                                                                                                                                             barrel medic.
                                                                                                                        BF640846
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       RESULT 10
BF640846/c
                                                                        DEFINITION
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truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20UM potassium
phosphate. RNA was prepared from above ground tissues."
a 162 c 133 g 161 t l others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 648)
Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library
                                                                                                                                                                                                                                                                                                                                           BG457226 648 bp mRNA EST 19-MAR-2001
NF101A05PLIF1035 Phosphate starved leaf Medicago truncatula cDNA
clone NF101A05PL 5', mRNA sequence.
341 agagctgttgttgttgttgtgaccatctgccattcttcctgttatgacagagcttgtg 400 il il il il il i
                                                                                      401 aactttaactgggactggggcaaagtcaatcccacctttatacaatgaattgctgaagag 460
                                             415 AGCTCAGTGGAGTTTGTTAATACCCATCTTCCAAAGCCTGCTTCTGTCNATTTGTTCATC 356
                                                                                                                                    355 TCATCCTCCATTCAGTTCTGTGCCCTTGCTGGAAAGTAATGTGATCATTTGGAGAAGAA 296
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                                                                                                                                                                               2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF101A05pt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mjharrison@noble.org
Insert Length: 648 Std Error: 0.00
Plate: 101 row: A column: 05
Seq primer: TCACACAGGAAACAGCTATGAC.
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The Samuel Roberts Noble Foundation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Harrison MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula
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                                                                                                                                                                                                                                                                                              RESULT 9
BG457226/c
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COMMENT
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KEYWORDS
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Location/Qualifiers

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Medicago truncatula

Medicago truncatula

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF642756 659 bp mRNA EST 19-DEC-2000
NF070F06INIF1058 Insect herbivory Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                     398 gigaactitaacigggacigggcaaagicaatcccacctitatacaaigaaitgcigaa 457
                                                                                                                                                                                                                                                                                                                                                                                                                          603 GGGAAGNTGAACTGTGACTGCGCGTAGTCAATGCCATCTTTCTCCTCAAATTTGACAGA 544
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                 DB 151; Length 654;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 GCGTCTGATGAAACCTCAAAGGGTCCTTCAATCTCGTCGAG 502
                                                                                                                                                                                                                                                                                                            6.6%; Score 33.8; DB 57.8%; Pred. No. 17; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                        Query Match 6.01
Best Local Similarity 57.88
Matches 59; Conservative
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//foctor: Lambda Zap; At the trifoliate stage, M.
/foctor: Lambda Zap; At the trifoliate stage, M.
//foctor: Lambda 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago truncatula
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 666)
Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF095F08PL1F1073 Phosphate starved leaf Medicago truncatula cDNA clone NF095F08PL 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 cttgtgaactttaactgggactggggcaaagtcaatcccacctttatacaatgaattgct 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 651 CCNGGNAAGCTGAACTGTGACTGCGGCGTAGTCAATGCCATCTTTCTCCTCAAATTTGAC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 153; Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 gaagaggccttttaaaaacttggagtgtgcattgtttatggaaggg 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     591 AGAGCCGTCTGATGAAACNTCAAAGGCTCNTTCAATCTCGTCGAG 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7336
Fax: 580 221 7380
                                                                                                                    1. .661
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Insert Length: 666 Std Error: 0.00
late: 095 row: F column: 08
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.6%; Score 33.8; D
56.2%; Pred. No. 17;
Live 0; Mismatches
                                          Seq primer: TCACACAGGAAACAGCTATGAC.
           Plate: 106 row: A column: 08
                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                              /tissue_type="leaf"
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BG457203/c
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/dev_stage="mature" and systemic leaves"
/dev_stage="mature" and systemic leaves from fully force="vector: Lambda 2ap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled." 2 others
1 (bases 1 to 659), Marris, A.R., Gonzales, R.A., Bell, C.J., Flores H.K., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
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Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
JH.R., Inman,J.T. Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
Contact: Harrison MJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                         Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Fal: S01 575 5191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 33.8; DB 151; Length 659; 57.8%; Pred. No. 17; Live 0; Mismatches 43; Indels 0;
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 661 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF070F061N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Insect herbivory"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Kkorthecomp.uark.edu
Insert Length: 659 Std Error: 0.00
Plate: 070 row: F column: 06
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Matches 59; Conservative
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Medicago.
period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20um potassium phosphate. RM was prepared from above ground tissues." 166 c 137 g 165 t
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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                                                                                                                                                                                                                                                                                                                                                                                                                                            398 gigaactitaacigggaciggggcaaagicaaicccaccittaiacaaigaaiigcigaa 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 gtgaactttaactgggactggggcaaagtcaatcccactttatacaatgaattgctgaa 457 | 111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 111
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/note="Vector: Lambda Zap; Contains a mixture of
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Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 gaggccttttaaaacttggagtgtgcattgtttatggaaggg 499
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/db_xref="taxon:3880"
/clone="NF022E07ST"
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Insert Length: 691 Std Error: 0.00
Plate: 022 row: E column: 07
Seg primer: TCACACAGGAAACACCTATGAC.
                                                                                                                                                                                                                                                                               6.6%; Score 33.8; Dilarity 57.8%; Pred. No. 18; Conservative 0; Mismatches
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The Samuel Roberts Noble Foundation
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Contact: Dixon RA
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/note="Vector: Lambda Zap; At the trifoliate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNa was prepared from above ground tissues."
                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 645)
Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
Liu,J., Scott,A.D., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
                                            BF637629 645 bp mRNA EST 19-DEC-2000 NF040D03PL1F1028 Phosphate starved leaf Medicago truncatula cDNA clone NF040D03PL 5', mRNA sequence.
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 645 546 Error: 0.00
Plate: 040 row: D column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.
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/db_xref="taxon:3880"
/clone="kr640003PL"
/clone=lib="Phosphate starved leaf"
/tissue_type="leaf"
/dev_stage="trifoliate"
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Job time: 7647 sec
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MMFLK1 AR005213 AR071705 125171 140602 HSDNAKDR AC021220 AR035121 AR030848 182807 AX060542 SC025 SC025	AC023682 AE004596 AE004596 AC05181 AC05182 AC065846 AC065664 AC005664 AC012073 AC012073	ACOUGUE ANDO ACE AYOO 422 AYOO 4226 AYOO 4226 AYOO 4226 ACO 20929 ACO 20929 ACO 12386 ACO 12386	kinase F 2 2 hordata; odentia; nd Breier in vivo in vivo gische ugerach generan in titiers us muscul Sv" lifiers us muscul Sv" lifiers in l096 e" liver' fetus"
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Direct Submission
Submitted (19-JUL-1995) C. Patterson, Harvard School of Public
Health, Cardiovascular Biology Lab, 677 Huntington Avenue, Building
2 Room 113a, Boston MA 02115, USA
Location/Qualifiers
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Patterson,C., Perrella,M.A., Hsieh,C.M., Yoshizumi,M., Lee,M.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning and functional analysis of the promoter for KDR/flk-1, a receptor for vascular endothelial growth factor J. Biol. Chem. 270 (39), 23111-23118 (1995)
                                                6636 ATTCGCTAGTGTGTGTAGCCGGCGCTCTCTTTCTGCCCTGAGTCCTCAGGACCCCAAGAGAG 6695
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/db_xref="G1:1129146"
/db_xref="SHISS-PROT:P35918"
/translation="MESKALLAVALWFCV"
173 c 185 g 101 t
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Patterson, C.
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Breier, G. and Risau, W.
REGULATORY SEQUENCE CAPABLE OF CONFERRING EXPRESSION OF A
HETEROLOGOUS DNA SEQUENCE IN ENDOTHELIAL CELLS IN VIVO AND USES
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MAX PLANCK GESELLSCHAFT (DE); BREIER GEORG (DE)
Location/Qualifiers
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100.0%; Pred. No. 1.3e-232;
ative 0; Mismatches 0;
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Sequence 1 from Patent WO9855638.
AX002124

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/organism="unidentified"

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2893 c 2863 g 3
916 TCTGTGCCCAGCGCGAGGTGCAGG 939
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NYK/FLK-1= platelet-derived growth factor receptor-related tyrosine kinase [mice, E10 embryonic neuroepithelium, mRNA, 4790 nt]. $553103.1 GI:264004
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0erichs,R.B., Reid,H.H., Bernard,O., Ziemiecki,A. and Wilks,A.F.
NYK/FLK-1: a putative receptor protein tyrosine kinase isolated
from E10 embryonic neuroepithelium is expressed in endothelial
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Location/Qualifiers
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                                                                             attegetagtgtgtageeggegetettetgeeetgagteeteaggaeeeeaagagag
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                                                               acagttccgggggtagtgggggagtgggcgtgggaaaccgggaaacccaaacctggtatcc
                             1 ACTICIACCAGAAACCGAGCIGCGICCAGAITIGCICICAGAIGCGACIIGCCGCCCGGC
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/gene="NYK/FLK-1"
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/organism="Mus sp."
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272. .4309
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VCDPKFHYDNTAGISHYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDSQTDSGMVL
ANTTLOITCRGGRDLDWLWPNAQRDSEERVLVTECGGGDSIFCKTLIIPRVVGNDTGA
YKCSYRDVDIASTVYVYVRDYRSPFIASVSDQHGIVYITTENKNKTVVIPCRGSISNLN
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Ullrich,A., Risau,W., Millauer,B., Gazit,A. and Levitzki,A.
FLK-1 is a receptor for vascular endothelial growth factor
Patent: US 5851999-A 1 22-DEC-1998;
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1. .5470
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Best Local Similarity 97.1%;
Matches 267; Conservative
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endothelial cell growth factor protein; Flk-1 gene; tyrosine kinase
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antfloitcrgqrdldmlwpnaqrdseervlytecgggdsifcktltiprycrddga
Yrcsyrdydiastvyvyvrdyrspflasysdqgivyitenknyvpcrgsisnln
Vslcaryperrevpdgnriswdseigftlpsymisyagmyfceakindetygsimyiv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/tissue_type="total embryo"
/clone_lib="lambda gtll mouse embryo Ell.5; Okayama Berg
mouse embryo E8.5"
/clone="7,17"
286. .4389
/gene="Flk-1"
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Millauer, B., Wizigmann-Voos, S., Schnurch, H., Martinez, R.,
Moller, N. P., Risau, W. and Ullrich, A.
High affinity VEGF binding and developmental expression suggest
Fik-1 as a major regulator of vasculogenesis and anglogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-JAN-1993) A. Ullrich, Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18A, 8033 Martinsried, FRG Differences between this sequence and that of Matthews et al: Sequence is 76 nucleotides longer at the 5' end Nucleotide insertions at positions 92, 130 and 4753 Nucleotide differences at positions 4810, 4813 and 4814.
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                                                                      711 geccagactgtgtecegeageegggataacetggetgaceegatteegeggacacegetg 770
                                                                                           189
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                                       Gaps
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                                         4;
 Length 5470;
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Score 169; DB 9;
Pred. No. 5.7e-34;
0; Mismatches 0;
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/organism="Mus musculus"
/strain="BALB/c"
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/gene="Flk-1"
/codon_start=1
18.3%;
98.2%;
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M.musculus Flk-1 mRNA
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Ullrich, A.
                                    Matches 213; Conservative
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RDVKPFPGTVAKMFLSTLTIESVTKSOGGETVCVASSGRMIKRNRTFVWHTKPPTAF
GSGMKSLVEATVGSGVRIPWKYLSYPAPDIKWYRNGPFIESNYTMIVGDELTIMEVTE
RDAGNYTVILTNPISMEKOSHWSZLVVNVPPQIGEKALISPMOSYQYGTWGTTCTVY
ANPPLIHIOWYRWOLERACSYRPGOTSPYACKEWRHVEDFOGGNKIEVTROYALIEGK
NKTVSTLVIQAANVSALYKCEAINKAGRGERVISFHVIRGPEITVQPAAQPTEQESVS
LLCTAANRYFENLTWYKLGSQATSVTHKGESITPVCKNIDALWKLUGTWESNSTNDILI
VAFONASLODGDVYCSAQDKKTKKRHCLKYQLIILERWAPMITGHENSTRDILI
VAFONASLODGDVYCSAQDKKTKKRHCLKYQLIILERWAPMITGHENGTWESNSTNDILI
VAFONASLODGDVYCSAQDKKTKKRHCLKYGLILERWAPMITGHENGTWESNSTNDILI
VAFONASLODGDVYCSAQDKKTKKRHCLKYGLILERWAPMITGHENGTWESNSTNDILI
VAFCNASCHPTPHTWFKNDSTLYBOSGIVLANGFRILLVIYURTVKRANGGELKTG
YLSIVMDPDELPLDERCERLPYDASKWEFF PRORKLICAVTSCROVIEGGOVIEDARGILK
TACKTVAVKMLKEGATREHRALMSELKILIHIGHHLNVYNLLGACTRFGGPLAVIV
EFCKFGNLSTYLRGKRNEFVPKSKGARFRGGKDYVGELSVDLKRRLDSITSSQSSAS
SGFVERESKSLSDVEREBRASEELKADFTLEHLICYSFOVAKGMEELSARCHIRDLAAR
NILLSEKNUVKICDFGLARDIYKDDDYRKGOARLEDNA
ORPSFERENVENLENGKRLDGREEDE
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EAGLLKMVDAAVHADSGTTLQLFSCLNGSGPVPAPPFFGGHERGAA"
1315 c 1448 g 1290 t
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Rattus norvegicus C-terminal truncated VEGF receptor-2/FLK-1 mRNA,
complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Wen,Y., Bdelman,J.L., Kang,T., Zeng,N. and Sachs,G.
Two functional forms of vascular endothelial growth factor receptor-2/Flk-1 mRNA are expressed in normal rat retina J. Biol. Chem. 273 (4), 2090-2097 (1998)
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Pred. No. 5.7e-34;
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Wen,Y., Edelman,J.L., De Vries,G.W. and Sachs,G.
Direct Submission
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1. .4016
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98.2%;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                      /note="growth factor receptor; receptor tyrosine kinase; lacks the carboxyl-terminal half of kinase domain and
                                                                                                                                                                                                                                                                              /product="C-terminal truncated VEGF receptor-2/FLK-1"
/protein_id="AAB97509.1"
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Two functional forms of vascular endothelial growth factor
receptor-2/Flk-1 mRNA are expressed in normal rat retina
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/organism="Rattus norvegicus"
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                                                                                                                                                                  Wen,Y., Edelman,J.L., De Vries,G.W. and Sachs,G.
Direct Submission
Direct Submitsion
Submitted (13-MAR-1997) Membrane Biology Lab, WLA/VA Medical
Center, 11301 Wilshire Blvd, Bldg. 113, Room 324, Los Angeles, CA
90073, USA
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/tissue_type="retina"
249:
/note="growth factor receptor; receptor tyrosine kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="VEGF receptor-2/FLK-1"
/protein_id="AAB97508.1"
/db_xref="G1:2098759"
J. Biol. Chem. 273 (4), 2090-2097 (1998)
98113170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
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718 ctgtgtcccgcagccgggataacctggctgacccgattccgcggacaccgctgcagccgc 777
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                                                                                                                                                                                                                                                            1 CTGTGTCCCGCAGCC-GGATAACCTGGCTGACCCGATTCCGCGGACACCGCTGCAGCCGC 59
                                                       Length 5391;
                                                                                      Indels
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Pred. No. 3.5e-30;
0; Mismatches 4;
                                                    Score 161; DB 94;
Pred. No. 7.2e-32;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1273
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Sequence 5 from patent US 5747651.
AR005213
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Sequence 5 from patent US 5912133.
AR071705
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                                                     17.4%;
98.1%;
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96.2%;
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Lemischka, I.R.
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                                                  Query Match
Best Local Similarity 98.1:
Matches 205; Conservative
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A receptor tyrosine kinase cDNA isolated from a population of enriched primitive hematopoietic cells and exhibiting close genetic linkage to c-kit

Proc. Natl. Acad. Sci. U.S.A. 88 (20), 9026-9030 (1991)
                                                                                                                                                                                                                Submitted (09-MAY-1991) C.T. Jordan, Princeton University, Dept. Molecular Biology, Washington Rd, Princeton, New Jersey 08544, USA 2 (bases 1 to 5391)
Matthews, W., Jordan, C.T., Gavin, M., Jenkins, N.A., Copeland, N.G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFSKFGNLSTYLRGKRNEFVPYKSKGARFRQGKDYVGELSVDLKRRLDSITSSQSSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGFVEEKSLSDVEEEEASEELYKDFLTLEHLICYSFQVAKGMETLASRKCIHRDLAAR
NILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VCDPKFHYDNTAGISHYLQNSKRKSRPVSVKTFEDIPLEEPEVKYIPDDSQTDSGMYL
ASEELKTLEDRNKLSPSFGGMMPSKSRESVASEGSNQTSGYQSGYHSDDTDTTYYSSD
EAGLLKMVDAAVHADSGTTLQLISCLNGSGPVPAPPPTPGNHERGAA"
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                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 5391)
                                   06-NOV-1991
                     MMFLK1 5391 bp mRNA ROD
MOUSE Flk-1 mRNA for a tyrosine kinase receptor.
X59397
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265. 4308
/gene="Fik-1"
/product="tyrosine kinase receptor"
1299 c 1422 g 1273 t
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                                                                                            Flk-1 gene; tyrosine kinase receptor
house mouse.
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1. .5391
/organism="Mus musculus"
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/db_xref="G1:50977"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C3H/He"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Flk-1"
208. .4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Flk-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Flk-1"
                                                                            X59397.1 GI:50976
                                                                                                                                                                                                      Direct Submission
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RESULT
MMFLK1
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718 ctgtgtcccgcagccgggataacctggctgacccgattccgcggacaccgctgcagccgc 777
04-DEC-1998
                                                                                                                                                                                                                                                                                                                                     4; Gaps
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                                                                                                                                                                                                                                                                                                  Length 5406;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                     Antibodies against tyrosine kinase receptor flk-1
Patent: US 5747651-A 5 05-MAY-1998;
10. .5406
PAT
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                                   1 (bases 1 to 5406)
Lemischka, I.R.
Method for isolating stem cells expressing flk-1 receptors
Patent: US 5912133-A 5 15-JUN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tyrosine kinase receptor human flk-2-specific antibodies Patent: US 5548065-A 5 20-AUG-1996;
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                                                                                                                                                                                      / Match 16.7%; Score 154.6; DB 9; Length 5406; Local Similarity 96.2%; Pred. No. 3.5e-30; Loss 201; Conservative 0; Mismatches 4; Indels 4;
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1298 c 1423 g
                                                                                                                 /organism="unknown"
1298 c 1423 q
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Lemischka, I.R.
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125171
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TITLE
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Direct Submission
Submitted (19-JUL-1995) C. Patterson, Harvard School of Public
Health, Cardiovascular Biology Lab, 677 Huntington Avenue, Building
2 Room 113a, Boston MA 02115, USA
Revised by [2]
Roises 1 to 1267)
Patterson, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1267)
Patterson, C., Perrella, M.A., Hsieh, C.M., Yoshizumi, M., Lee, M.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cloning and functional analysis of the promoter for KDR/flk-1, a receptor for vascular endothelial growth factor J. Biol. Chem. 270 (39), 23111-23118 (1995)
                                                                                                                                                                                                                                    1 (bases 1 to 5406)
Lemischka,1.R.
Nucleic acids encoding soluble human FLK-2 extracellular domain
Patent: US 5621090-A 5 15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GCCTGGAGCCAGGGCGCCGGTG-CCCCCGCTCTCCCCCGGTCTTGCGCTGCGGGGCCGGAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            838 accgcctctgtgacttctttgcgggccagggacggagaaggagtctgtgcctgag-aact 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ACCGCCTCTGTGACTTCTTTGCGGCCAGGAGAAGGAGAAAGGAGTCTGTGCCTGAGAAACT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           718 ctgtgtcccgcagccgggataacctggctgacccgattccgcgggacaccgctgcagccgc 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTGTGTCCCGCAGCC-GGATAACCTGGCTGACCCGATTCCGCGGACACCCGTGCAGCGGC 59
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                                                                                                    13-MAY-1997
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                                                                                                    PAT
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 154.6; DB 10
Pred. No. 3.5e-30;
0; Mismatches 4;
                                                                                      140602 5406 bp DNA
Sequence 5 from patent US 5621090.
140602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 GGCTCTGTGCCCAGGCGCAGGTGCAGG 207
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. 5406
                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                        1423 g
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Best Local Similarity 96.2%;
Matches 201; Conservative (
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Patterson, C.
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                                                                                                                                                   I40602.1 GI:2082894
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                                                                                                                                                                                                      Unknown.
Unclassified.
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Direct Submission
Submitted (14-JAN-1996) C. Patterson, Harvard School of Public
Health, Cardiovascular Biology Lab, 677 Huntington Avenue, Building
2 Room 113a, Boston MA 02115, USA
On Jan 15, 1996 this sequence version replaced gi:1019387.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 110; DB 93; Length 1267;
Pred. No. 2.3e-18;
0; Mismatches 300; Indels 66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 caaagcaccataaaacaaaacttccaagtactgac-caactcactgcaagtttgtgccc 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 CAAAATACCCTTATACAAAAACCAAAACTACTGGCAGGAGTCGCTGCCAGCTTGCGACCC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 tcccttgggactttcagtgcagcggagagagagttctgcacttgcaggctcctaatgag 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 ggcgcagtgggcctcgt---gtttctggtgatgcttcccaggttgctggggggcagcagt 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705 ----ctgaaagcccagactgtgcccgcagcgggataacctggctgacccgattccgc 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 ggaccccaagagagtaagctgtgtttccttagatcgcgcggaccgctacccggcagga-- 704
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                                                                                                                                                                                                                                                                                    /product="vascular endothelial growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 AAAGTTGTTGCTCTGGGATGTTCTCTCGGGCGACTTGGGGCCCCAGCGCAGTCCAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="cAA61916.1"
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/translation="MQSKVLLAVALMICVETRAASV"
                                                                                                                             organism="Homo sapiens"
                                                                                                                                          'db_xref="taxon:9606"
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                                                                                                                                                                                gene="KDR/flk-1"
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/gene≕"KDR/flk-1"
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56.0%;
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Submitted (15-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 214348)
Waterston, R.H.
                                                                                                                                     972 CIGCGCIGCGGGGIGCCGCGAGIICCACCICCGCGCCICCTICTICTAGACAGGCGCIGGG 1031
-gogoataccgcctctgtgacttctttgcgggccagggac--gg
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 4 clone RP11-530117, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently * consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Nov 15, 2000 this sequence version replaced g1:9309528.
                                                                                                                                                                               Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 161000; agarose-fp
Insert size: 210648; sum-of-contigs
Quality coverage: 4.96 in Q20 bases; agarose-fp
Quality coverage: 4.62 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 1584 bp in length of unknown length contig of 2510 bp in length gap of unknown length contig of 2130 bp in length gap of unknown length gap of unknown length contig of 3320 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- Project Information ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-primer ET: 87% of reads
Chemistry: Dye-terminator Big Dye; 13% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 195065 bases at least Q40
Consensus quality: 200600 bases at least Q30
Consensus quality: 203756 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 878
Sequencing vector: plasmid; 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: H_NH0530117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Center
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, 38 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT
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Direct Submission
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us-09-445-201-1_copy_6036_6959.rge

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9944: gap of unknown 14101: contig of 41015 14201: gap of unknown 21279: contig of 7076 21379: gap of unknown 31346: gap of unknown 40526: contig of 908 40626: gap of unknown 52862: contig of 10225 15962: gap of unknown 66090: contig of 10226 129319: contig of 1646 8259: gap of unknown 104797: contig of 1646 129319: contig of 2441129319: contig of 244108	176512 176611: gap of unknown length 176612 17766: contig of 1055 bp in length 17766: gap of unknown length 17766: 177766: gap of unknown length 17767 178997: contig of 1231 bp in length 179098 180242: contig of 1231 bp in length 179098 180242: contig of unknown length 180243 180242: contig of 1100 bp in length 18143 181242: gap of unknown length 181543 182642: contig of 1100 bp in length 18722 184165: contig of 1100 bp in length 18722 188724: gap of unknown length 18722 188724: contig of 1247 bp in length 185513: contig of 1247 bp in length 186513: gap of unknown length 18722 188724: contig of 1509 bp in length 18722 188724: contig of 1859 bp in length 189783: gap of unknown length 189783: gap of unknown length 191313: 191412: gap of unknown length 191313: 191412: gap of unknown length 192838: 191412: gap of unknown length 192938: 194117: contig of 1430 bp in length 194218: gap of unknown length 194218: gap of unknown length 194218: gap of unknown length 19744: gap of unknown length 19744: gap of unknown length 19744: gap of unknown length 197845: gap of unknown length 197865: gap of unknown length 197865: gap of unknown length 1978605: gap of unknown length 197865: gap of unknown length 1978665: gap of unknown leng	204591 206676: contig of 208 206577 206776: gap of unknow 206777 208703: contig of 202 208804 208803: contig of 202 208804 208903: gap of unknow 208904 210597: contig of 169 212098 212097: contig of 140 212098 212197: gap of unknow 212098 21210000000000000000000000000000000000
*****	*********	**** PEATURES SOUICE

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        Matches
        148;
        Conservative
        0;
        Mismatches
        65;
        Indels
        7;
        Gaps
        3;

        QY
        711
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

June 21, 2001, 18:06:24; Search time 346.98 Seconds Run on:

(without alignments)
1554.597 Million cell updates/sec

US-09-445-201-1_COPY_6036_6959 924 Title: Perfect score:

gaagttcacaaccgaaatgt.........tgcccagcgcgaggtgcagg 924 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

678276 seqs, 291890651 residues Searched:

Total number of hits satisfying chosen parameters:

1356552

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

N_Geneseq_0401:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

flk-1 cDNA sequenc Murine flk-1 cDNA. Human flk-1 coding Murine flk-1 cDNA. Flk1 receptor prot Mouse flk-1 cDNA. Mouse KDR/flk-1 pr Sequence of murine Murine foetal live Murine flk-1 cDNA. Mouse endothelial Description SUMMARIES V84274 T60766 Q64049 X77516 Q29957 Q81014 079070 040916 138735 053504 035251 20 118 117 117 118 119 Match Length DB 5406 5406 5406 5406 5406 5404 5406 12845 100.0 40.5 116.7 116.7 116.7 116.7 116.7 116.7 Query 154.6 154.6 154.6 154.6 154.6 154.6 Score 169 Result

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ALIGNMENTS

V84274 standard; DNA; 12845 BP 12-APR-1999 (first entry) RESULT V84274

Flk-1; endothelial growth factor receptor-2; VEGF; transcription; Mouse endothelial growth factor receptor-2 gene Flk-1 5' region.

endothellum; enhancer; vascular disease; angiogenesis; cancer; diabetic retinopathy; rheumatoid arthritis; wound healing; vulnerary; atherosclerosis; tumour; neuronal disorder; therapy; diagnosis; mouse; ss.

Mus sp

Location/Qualifiers 6036..6959 /codon_start~ 6960 7027..10632 ıg÷ a ...7026 /*tag= b /number= 1 /number= /*tag* 6661..70 /*tag= promoter intron exon Key

/note= "DNA sequences comprising nucleotides 8260-10560, 8336-10608 and/or 10094-10608 are specifically claimed in Claim 3b" /note= "GATA/PEA3 consensus binding site" /*tag= protein_bind

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This 12.8 kb DNA sequence spans the region from -6.65 kb relative to the transcriptional start site to +6.15 (located in the third exon) of the murine endothelial growth factor (VEGF) receptor-2 gene Filt. This portion of the Filt.1 gene was isolated from the liver of mouse strain 129/SvJ by screening a phage library of liver genomic DNA in vector lambda FixII. Sequences within the 5'-flanking region of the gene, in combination with sequences located within the first intron, specifically and reproducibly target expression of heterologous DNA to andioloblasts during early stages of vascular equal expression of the vasculature of postnatal mice. The regulatory sequences of the first intron also function as an autonomous endothelium specific enhancer when fused to a autonomous endothelium specific enhancer when fused to a suconomous endothelium specific enhancer. This Filt-1 intron enhancer contains several potential binding sites for transcription factors of the Ets and GATA families. The invention provides a new claimed recombinant DNA (1) comprising at least one regulatory sequence from an intron of the Fik-1 gene, or its homologue, to control expression in endothelial cells, in vivo, linked to (b) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA containing heterologous sequence controlled by endothelial cell specific regulator - from the Flk-1 gene, used to treat, prevent or diagnose vascular disease, tumours, also to screen for transcriptional regulators
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these, or transformed cells, are used to identify agents (A), obtential pharmaceuticals, that suppress, activate or enhance transcription of genes in endothelial cells. (I), vectors and (A) are used to direct or prevent (for antisense sequences) expression of genes specifically in endothelial cells. (I), vectors and (A) are used to direct or prevent (for antisense sequences) expression of genes specifically in endothelial cells, eg. for treating angiogenesis, cancer, diabetic retinopathy, rheumatoid arthritis etc., and in wound healing, particularly for treating vascular specifically atherosclerosis), tumours and neuronal disorders. They may also be used to induce vascular disease in the transgenic animals or diagnostically, particularly for studying (mal)function, interactions and unregulated expression of endothelial products. (I) provide specific modulation of gene expression in endothelial cells, at all stages of development.
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Matches 924; Conservative
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cell specific transcription of operably linked polypeptide-encoding
              \begin{tabular}{ll} KDR/flk-1; promoter; regulation; endothelial cell; transcription; gene therapy; treatment; specific; ds. \\ \end{tabular}
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"potential cis-acting element (E Box)"
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/note= "potential cis-acting element (GATA)"
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                                                                                                                                                                        Mouse KDR/flk-1 promoter bases (-295) to 205.
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Bases (-225) to (-164) of the present sequence, the KDR/flk-1
promoter, regulate the endothelial cell specific transcription of
a polypeptide encoding sequence to which it is operably linked,
e.g. tissue plasminogen activator, p21 cell cycle inhibitor,
nitric oxide synthase, interferon gamma or atrial natriuretic
polypeptide. The products can be used in gene therapy, e.g. to
inhibit or enhance angiogenesis, or to treat tumours or vascular
diseases, such as arteriosclerosis or inflammatory diseases, e.g.
rheumatoid arthritis or diabetic retinopathy. They can also be
used to promote wound healing, e.g. healing of broken bones,
burns, diabetic ulcres and traumatic or surgical wounds, or to
treat peripheral vascular disease, atherosclerosis, cerebral
vascular disease, hypoxic tissue damage, e.g. hypoxic damage to
heart tissue, diabetic pathologies, such as chronic skin lesions,
or coronary vascular disease. They can also be used to treat
patients who have, or have had, translent ischemic attacks,
or poor circulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 acttccaccagaaaccgagctgcgtccagatttgctctcagatgcgacttgccgccggc 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human amouse KDR/fik-1 DNA was obtained, and DNA elements important for basal expression in endothelial cells identified using a series of luciferase reporter plasmids containing serial 5 deletions through the promoter region. The deletion analysis indicated that 3 sequences in the 5' flanking region of the gene contain elements important for expression in endothelial cells. The promoter sequence which regulates endothelial cell specific transcription was found to comprise nucleotidses (-225) to (-164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 acagttccggggtagtgggggagtgggcgtgggaaaccgggaaacccaaacctggtatcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.5%; Score 374.2; DB 18; Length 500; Best Local Similarity 98.8%; Pred. No. 7.3e-97; Matches 398; Conservative 0; Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 tggagccagggcgccggtgccccgcgctctccccggtcttgcg 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 500 BP; 85 A; 158 C; 166 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the KDR/flk-1 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    064049 standard; DNA; 5470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               064049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        064049
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11-DEC-1996 (first entry)
            T38735;
                                                                                                                                                                                                                    Key
 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A receptor tyrosine kinase cDNA, designated foetal liver kinase I (Flk-1), was cloned from mouse cell populations enriched for haematopoletic stem and progenitor cells. The nucleotide coding sequence and deduced As sequence of the murine Flk-1 gene is depicted in Q64049/R54046) and has been described in Matthews et al., 1991, proc. Matl. Acad. Sci. USA, 88:9026-9030. The murine Flk-1 gene was isolated by performing a PCR using two degenerate oiling primer pools that were designed on the basis of highly conserved sequences within the kinase domain of receptor tyrosine kinases (Hanks et al., 1988). Based on AA homology, this receptor is a member of the type III subclass of RTKS (Ullrich and Schlessigner) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -cagocgoggctggagccagggcgccggtgcccgcgctctccccggtcttgcgctgcgg 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 acagccgcggctggagccagggcgccggtgccccgcgctctccccggtcttgcgctgcgg 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gggcgcataccgcctctgtgacttctttgcgggccagggacggaggaggaggagtctgtgcct 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Flk-1, a tyrosine kinase receptor for vascular endothelial growth factor - used to express recombinant Flk-1 for screening for ligands useful for modulating vasculogenesis and anglogenesis e.g. for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin-like repeats in their extracellular domains.
Sequence of murine genomic foetal liver kinase 1 (Flk-1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.3%; Score 169; DB 15; Length 5470; 98.2%; Pred. No. 3.8e-38; tive 0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5470 BP; 1417 A; 1324 C; 1440 G; 1289 T; 0 other;
                            Foetal liver kinase; receptor tyrosine kinase; ss.
                                                                                                                                                                                                                                                                              (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gag-aactgggctctgtgccca-gcgcgaggtgcagg 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 50-56; 99pp; English.
                                                                                     Location/Qualifiers 286..4386
                                                                                                                                                                                                                                                                                                         Millauer B, Risau W, Ullrich A;
                                                                                                                                                                                                                                  92US-0975750.
                                                                                                                                                                                                      93WO-EP03191
                                                                                                                   /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                     WPI; 1994-183501/22.
P-PSDB; R54046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                         Mus musculus
                                                                                                                                                                                                      15-NOV-1993;
                                                                                                                                                                                                                                   13-NOV-1992;
                                                                                                                                                                                                                                                26-MAR-1993;
                                                                                                                                              WO9411499-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213;
                                                                                                                                                                           26-MAY-1994
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Matches 21
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                                                                                      Key
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4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells, and to isolate positive cells. The antibodies can also be used as, or to obtain ligands, which stimulate the proliferation and/or differentiation of stem cells. The ligands can be used, e.g. for treating anaemia, or bone marrow damage resulting from cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays, for isolating haematopoietic stem cells expressing receptor and for obtaining ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes murine foetal liver kinase 1 (flk-1), a protein tyrosine Kinase. Isolated antibodies, pref. monoclonal, raised against the extracellular portion of flk-1 can be used to assay for flk receptors on the surface of haematopoietic stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 5404;
                                             Murine; foetal liver kinase 1; flk-1; protein tyrosine kinase;
                                                                    monoclonal, antibody, extracellular domain, receptor assay, haematopoietic stem cell; ligand; stimulation; proliferation; differentiation; treatment; anaemia; bone marrow damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.7%; Score 154.6; DB 17; Length 96.2%; Pred. No. 4.7e-34; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 51-62; 50pp; English.
                                                                                                                                                                                                                                           Location/Qualifiers
208..4311
                                                                                                                                                cancer chemotherapy; radiation; ds.
Murine foetal liver kinase 1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-0977451.
91US-0679666.
91US-0728913.
91US-0793065.
91US-0813593.
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92US-0975049.
93US-0055269.
94US-0252517.
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                                                                                                                                                                                                                                                                                                                                           /*tag= b
265..4308
                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
                                                                                                                                                                                                                                                                                                /*tag= a
208..264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; T38735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lemischka IR;
                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1991;
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24-DEC-1991
                                                                                                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
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T38735 standard; cDNA; 5404 BP

RESULT T38735 ID T3

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This invention describes a novel method of isolating cells expressing fetal liver kinase 1 (flx1) receptors on their surface and comprises binding the cells to a polyclonal or monoclonal antibody specific to the Fix-1 receptor and isolating the cells that have bound to the antibody. The method can be used to isolate hematopoietic stem cells in any manmal but preferably a rat, mouse, rabbit or human. The proteins of the invention belong to the receptor protein family. This sequence encodes the murine flx-1 protein which is used in the method of the
                   Murine; flk-2; flk-1; cell isolation; fetal liver kinase; receptor; monoclonal; polyclonal; antibody; tyrosine kinase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolating hematopoietic cells expressing fetal liver kinase 1
                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "flk-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 59pp; English.
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910S-0728913.
910S-0793065.
910S-0813593.
920S-0906397.
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93US-0055269.
94US-0252498.
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P-PSDB; Y08618.
                                                                                                                                                                                                                                                                                                                                                                                                   Murine flk-1 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lemischka IR;
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28-JUN-1991;
15-NOV-1991;
24-DEC-1991;
26-JUN-1992;
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30-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors
                                                                                                                                                                                                                                                                                                                          X77516;
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                                                                                                                                                                                                                                                'n
778
                                                                       838
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Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 T; 0 other;

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837
                                                                                                                                           838 accgcctctgtgacttctttgcgggccagggacggagaaggagtctgtgcctgag-aact 896
                                               777
                       Gaps
                                            The murine foetal liver kinase (flk) -1 clone was isolated by standard PCR techniques from stem-cell receptor-contg. tissue cDNA libraries. Sultable tissues include foetal liver, spleen or thymus cells or adult marrow or brain cells. The PCR primers used are based on known sections of the flk-1 gene. The murine flk-1 clone may be used in a vector to transform haematopoietic cells. The thymidine kinase encoded by flk-1 is expressed in primative but not mature
                                                                                            Thymidine kinase; TK; haematopoietic; stem cells; proliferation; differentiation; progenitor cells; foetal liver kinase; ss.
 Length 5404;
                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stimulating proliferation and/or differentiation of primitive mammalian haematopoietic stem cells - using ligand that binds thymidine kinase and flk-1 and flk-2
                       Indels
 20;
Score 154.6; DB 2 Pred. No. 4.7e-34;
                       0: Mismatches
                                                                                                                                                                                        897 gggctctgtgccca-gcgcgaggtgcagg 924
                                                                                                                                                                                                              179 gggctctgtgcccaggcgcgaggtgcagg 207
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
208..4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Fig 2; 94pp; English.
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16.78;
96.28;
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                                                                                                                                                                                                                                                                                                                           (first entry)
         Local Similarity 96.2
les 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                flk-1 cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09217486-A.
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 Query Match
                                                                                                                                                                                                                                                                                                  029957;
                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                               029957
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haematapoietic cells. Ligand binding to the TK may be prepd. which can stimulate proliferation and/or differentiation of primative haematapoietic cells in vivo. The ligands can stimulate the proliferation of additional primitive stem cells, differentiation into see also Q29954-6.
                                                                                                                                                                 ctgtgtcccgcagccgggataacctggctgacccgattccgcggacaccgctgcagccgc 777
                                                                                                                                                                                                              accgcctctgtgacttctttgcgggccagggacggaaggagtctgtgcctgag-aact 896
                                                                                                                                                                                                                                                                                119 accgcctctgtgacttctttgcgggccagggacggagaaggagtctgtgcctgagaaact 178
                                                                                                                                            Gaps
                                                                                                                                                                                       1 ctgtgtcccgcagcc-ggataacctggctgacccgattccgcggacacccgtgcagccgc 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor protein tyrosine kinase; pTK family; foetal liver kinase; mflk; primitive; totipotent; haematopoietic cell; stem cell; proliferation; stromal cell; ds.
                                                                                                                                             4;
                                                                                                                     DB 13; Length 5406;
                                                                                   Sequence 5406 BP; 1412 A; 1294 C; 1427 G; 1273 T; 0 other;
                                                                                                                                           Indels
                                                                                                                    Score 154.6; DB 13;
Pred. No. 4.7e-34;
0; Mismatches 4;
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/note= "hydrophobic leader"
                                                                                                                                                                                                                                                                                                           gggctctgtgccca-gcgcgaggtgcagg 924
                                                                                                                                                                                                                                                                                                                       179 gggctctgtgcccaggcgcgaggtgcagg 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= mflk-1
208..264
                                                                                                                                                                                                                                                                                                                                                                                        Q53504 standard; cDNA; 5406 BP
                                                                                                                  16.78;
96.28;
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910S-0793065.
910S-0813593.
920S-0906397.
920S-0975049.
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                                                                                                                  Query Match 16.7
Best Local Similarity 96.2
Matches 201; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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12-NOV-1992;
19-NOV-1992;
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                                                                                                                                                                                                                                                           838
                                                                                                                                                                                                                                                                                                           897
                                                                                                                                                                                                                                                                                                                                                                   RESULT
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119 accgcctctgtgacttctttgcgggccagggacggagaggagtctgtgcctgagaaact 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; receptor; protein; tyrosine kinase; pTK; primitive; mammalian; hematopoietic cell; pHC; mature; mHC; fetal; liver kinase 2; flk-1; liver; spleen; thymus; adult; brain; marrow; thymocyte; subset; multipotential; T-lymphoid; lineage; stomach; kidney; lung; heart; intestine; muscle; lymph node; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                      1 ctgtgtcccgcagcc-ggataacctggctgacccgattccgcgggacacccgtgcagccgc 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                        838 accgcctctgtgacttctttgcgggccagggacggagaggagtctgtgcctggg-aact
                                                                                                                                                      Nucleic acid sequences coding for murine flk-2 and specified subfragments of it are claimed. The murine flk-1 coding sequence (i.e. 053504) is also disclosed. The flk polypeptides are receptor protein tyrosine kinases which are expressed only in
                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                        Length 5406;
                                                                                     receptor flk-2 - encoding mammalian receptor protein tyrosine kinases expressed in primitive haematopoietic cells
                                                                     Isolated nucleic acid molecules of hematopoietic stem cell receptor flk-2 - encoding mammalian receptor protein twros
                                                                                                                                                                                                                                          Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                     Score 154.6; DB 14;
Pred. No. 4.7e-34;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                           Disclosure; Fig 2; 60pp; English
                                                                                                                                                                                                                 primitive haematopoietic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q35251 standard; cDNA; 5406 BP.
                                                                                                                                                                                                                                                                                     16.7%;
96.2%;
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91US-0813593.
92WO-US02750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human flk-1 coding sequence.
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                                                                                                                                                                                                                                                                                                               Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208..4311
                             WPI; 1993-405021/50.
P-PSDB; R44996.
                                                                                                                                                                                                                                                                                                  Best Local Similarity
Lemischka IR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1991;
24-DEC-1991;
02-APR-1992;
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RESULT 10
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                                                                                                                                            This sequence encodes a human receptor protein tyrosine kinase which belongs to a new functional class of protein tyrosine kinases (pTKS). However, this pTK is not in the same class as fik-2. pTKS in the same class as fik-2 pTKS in the same class as fik-2 but not in mature hematopoietic cells (mHC). This gene is expressed in more mature hematopoietic cells. The protein encoded by this sequence is an example of a receptor pTK and is called fetal liver kinase 1 (fik-1). Fik-1 is expressed in fetal liver, spleen, thymus, brain, stomach, kidney, lung, heart and intestine, and adult brain, kidney, heart, spleen, lung, muscle, marrow and lymph nodes.
                                                                                                                                                                                                                                                                                                                                         60 ggctggagccagggcgccggtg-cccgcgctctccccggtcttgcgctgcggggggcgat 118
                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine; receptor; protein; tyrosine kinase; pTK; flk-1; flk-2; adult; family; primitive; hematopoietic cell; mature; fetal; liver; spleen; thymus; brain; stomach; kidney; lung; heart; intestine; bone marrow;
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           838 accgcctctgtgacttctttgcgggccagggacggagaaggagtctgtgcctgag-aact
                                                                                     - allows
                                                                                                                                                                                                                                                                                               / Match 16.7%; Score 154.6; DB 14; Length 5406; Local Similarity 96.2%; Pred. No. 4.7e-34; nes 201; Conservative 0; Mismatches 4; Indels 4;
                                                                                                                                                                                                                                                                Sequence 5406 BP; 1412 A; 1299 C; 1422 G; 1273 T; 0 other;
                                                                                Nucleic acid encoding receptor protein tyrosine kinase -development of ligands to stimulate proliferation and/or differentiation of mammalian haematopoietic stem cells
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/note= "Hydrophobic leader sequence"
265..4308
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                                                                                                                          Claim 10; Fig 2; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q40916 standard; cDNA; 5406
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                                                                                                                                                                                                                                                                                                                     Matches 201; Conservative
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208..264
         (UYPR-) UNIV PRINCETON
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                                                   WPI; 1993-036323/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine flk-1 cDNA.
                                                              P-PSDB; R31377
                               Lemischka IR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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accgcctctgtgacttctttgcgggccagggacggaaggaggagtctgtgcctgag-aact 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the murine receptor protein tyrosine kinase (PTK), flk-1. This pTK is not in the same family as flk-2 (see also 040914-15) as it is expressed in primitive hematopoietic cells and also in mature hematopoietic cells. flk-1 is expressed in fetal liver, spleen, thymus, brain, stomach, kidney, lung, heart and intestine and adult brain, bone marrow, kidney, heart, spleen, lung,
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                                                                                                                                                                                                                                                                                                                       Totipotent haematopoietic stem cell receptors, their ligands an DNA sequences – for treating anaemia(s) and bone marrow damage due to e.g. cancer chemotherapy or radiotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 5406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 154.6; DB 14; Length Pred. No. 4.7e-34; O: Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flk1 receptor protein-tyrosine-kinase cDNA
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96.2%;
                                                                                                                             910S-0793065
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                                                                                    92WO-US09893
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Matches 201; Conservative
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                                                                                                                                                                      (UYPR-) UNIV PRINCETON
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P-PSDB; R37504.
                                                                                                                                                                                                                 Lemischka IR;
                                                                                                                             15-NOV-1991;
                                                                                 16-NOV-1992;
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WO9310136-A.
                                        27-MAY-1993
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                                                                                                                                                                                                                                                                                                                             The sequence corresponds to a cDNA encoding a mouse Flk1 (fetal liver kinase) receptor protein-tyrosine-kinase. Flk1 is expressed in both primitive and mature hematopoietic cells, and in other tissues. The gene product is useful in isolation of receptor ligands, which have applications in diagnosis of bone marrow disorders and in stimulating proliferation and/or differentiation
/product= Flk1 receptor protein-tyrosine-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.7%; Score 154.6; DB 16; Length 5406; 96.2%; Pred. No. 4.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fetal liver kinase-1; flk-1; protein tyrosine-kinase receptor; hematopoiesis; stem cell; ds.
                                                                                                                                                                                                                                                            Ligand for receptor protein tyrosine kinase – useful for th
stimulation of primitive haematopoietic stem cells causing
proliferation and/or differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
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0; Mismatches 4
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                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 131pp; English.
                                                                                                                                    93US-0080244.
93US-0081508.
93US-0157490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q79070 standard; cDNA; 5406
                                                                                                              94WO-US06944
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                    /*tag= b
265..4308
/*tag= c
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Best Local Similarity 96.2
Matches 201; Conservative
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                                                                                                                                                                                 (UYPR-) UNIV PRINCETON.
                                                                                                                                                                                                                             WPI; 1995-052014/07.
P-PSDB; R67817.
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                                                                                                                                                                                                       Lemischka IR;
                                                                                                                                                21-JUN-1993;
23-NOV-1993;
                                                                                                                                      18-JUN-1993;
                                                                  W09500554-A
                                                                                         05-JAN-1995
           sig_peptide
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119 accgcctctgtgacttctttgcgggccagggacggaggaggaggagtctgtgcctgagaaact 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ctgtgtcccgcagcc-ggataacctggctgacccgattccgcggacacccgtgcagccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     838 accgcctctgtgacttctttgcgggccagggacggagaggagtctgtgcctgag-aact
                                                                                                                                                                                                                                                                                                                                                                                Murine flk-2 receptor protein tyrosine kinase - used to stimulate proliferation and/or stimulation of primitive mammallan haematopoietic stem cells in vitro or in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.7%; Score 154.6; DB 16; Length 5406; 96.2%; Pred. No. 4.7e-34; Live 0; Mismatches 4; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 gggctctgtgcccaggcgcgaggtgcagg 207
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                               Location/Qualifiers
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91US-0793065.
91US-0813593.
92US-0906397.
92US-0975049.
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                                                                             /*tag= b
265..4308
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                                            208..4311
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208..264
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                                                                                                                                                                                                                                                                                                                         Lemischka IR;
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12-NOV-1992;
19-NOV-1992;
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                                                                                                                                                                        02-APR-1991;
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24-DEC-1991;
                                                                                                                            US5367057-A.
                                                                                                                                                                                                                                                                            30-APR-1993
                                                                                          mat_peptide
                                                                  sig_peptide
                                                                                                                                                  22-NOV-1994
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This sequence encodes the murine fetal liver kinase I (flk-1). flk-1 is a receptor protein tyrosine kinase (pTK). flk-1 is found in the same organs as flk-2 (see also T72117-18) as well as in fetal brain, stomeoth, kidney, lung, heart and intestine, and in adult kidney, heart, spleen, lung, muscle and lymph nodes. flk-1 is not a member of the manure hematopoietic as flk-2, as flk-1 may be found in more mature hematopoietic cells. The invention concerns a recombinant nucleic acid, preferably mRNA, which encodes a protein containing only the extracellular domain of human flk-2 and lacking the flk-2 intracellular domain. The resultant protein represents a soluble form of flk-2 which is used to isolate specific ligands for flk-2. These ligands can be used to stimulate proliferation and/or differentiation of mammalian hemmetopoietic stem cells, in vivo or in vitro, e.g. for
                                                                               Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase; ppTK; liver; spleen; thymus; adult; brain; bone marrow;primitive portion; haematopoietic hierarchy; extracellular domain; soluble form; ligand; proliferation; differentiation; mammalian; haematopoietic stem cell; macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of macrocytic or aplastic anaemia or bone marrow damage caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein containing the extracellular domain of human flk-2 - used for identification of primitive haematopoietic cell proliferation and differentiation stimulatory ligands, e.g. for treating anaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                /product= Murine_flk-1
                                                  Murine flk-1 receptor coding sequence.
                                                                                                                                                                                                                           Location/Qualifiers 208..4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment or radiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                      910S-0679666.
910S-0728913.
910S-0793065.
910S-0813593.
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                19-AUG-1997 (first entry)
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                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lemischka IR;
                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-1991;
                                                                                                                                                                                                                                                                                                                US5621090-A.
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KDR/flk-1; promoter; regulation; endothelial cell; transcription;
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/note= "potential cis-acting element (Sp1/Ap2)"
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/note= "potential cis-acting element (E Box)"
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/note= "potential cis-acting element (E Box)"
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/note= "potential cis-acting element (E Box)"
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/note= "potential cis-acting element (E Box)"
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"potential cis-acting element (GATA)"
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964..969
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note= "potential cis-acting element (Ap2)"
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"transcription start site"
                                                                                                                                                                                 Human KDR/flk-1 promoter bases (-780) to 487.
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note= "potential cis-acting
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/note= "potential cis-acting
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/note= "potential cis-acting
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/note= "potential cis-acting
                                                                                                                                                                                                                                                    gene therapy; treatment; specific; ds
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1000..992
/*tag= a
                                           T60765 standard; DNA; 1267
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                                                                                                                                                                                                                                                                                             Homo sapiens
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RESULT 13
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Score 154.6; DB 18 Pred. No. 4.7e-34;); Mismatches 4;

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Matches 201; Conservative

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Similarity

Query Match Local

16.7%; 96.2%;

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291 gtgcagcggcgaagagagttctgcacttgcaggctcctaatgagggcgcagtgggcctcg 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Important for basal expression in endothelial cells identified using a series of luciferase reporter plasmids containing serial 5' deletions through the promoter region. The deletion analysis indicated that 3 sequences in the 5' flanking region of the gene contain elements important for expression in endothelial cells. The promoter sequence which regulates endothelial cells. The promoter sequence which regulates endothelial cells specific of the RDR/filk-1 promoter.
                                                                                                                                                                                                                                                                                                                                              KDR/flk-1 promoter sequence - useful for regulation of endothelial
cell specific transcription of operably linked polypeptide-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyctcaycycccyttaccyaytactttttatttaccayaaacaaattyttyctctyy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bases (-225) to (-164) of the present sequence, the KDR/flk-1 promoter, regulate the endothelial cell specific transcription of a polypeptide encoding sequence to which it is operably linked, e.g. tissue plasminogen activator, p21 cell cycle inhibitor, nitric oxide synthase, interferon gamma or atrial natriuretic polypeptide. The products can be used in gene therapy, e.g. to inhibit or enhance angiogenesis, or to treat tumours or vascular diseases, such as arteriosclerosis or inflammatory diseases, e.g. rheumatoid arthritis or diabetic retinopathy. They can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 cagcgctcctggtgatgctccccaaatttcggggaccggcaagcgattaaatcttggagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to promote wound healing, e.g. healing of broken bones, burns, diabetic ulcers and traumatic or surgical wounds, or to treat peripheral vascular disease, atherosclerosis, cerebral vascular disease, hypoxic tissue damage, e.g. hypoxic damage to heart tissue, diabetic pathologies, such as chronic skin lesions, or coronary vascular disease. They can also be used to treat patients who have, or have had, transient isohemic attacks, vascular graft surgery, balloon angioplasty, frostbite, gangrene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.6%; Score 107.6; DB 18; Length 1267; 57.5%; Pred. No. 6.1e-21; tive 0; Mismatches 234; Indels 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1267 BP; 238 A; 372 C; 394 G; 263 T; 0 other;
                                                                                                                                                                                                                                                            Haber E, Lee M, Patterson-Winston C;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 45; 70pp; English.
                                                                                                      96WO-US10725.
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Matches 400; Conservative
                                                                                                                                                                                                                 (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                     WPI; 1997-087384/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or poor circulation
               WO9700957-A1
                                                                                                      21-JUN-1996;
                                                                                                                                                 18-DEC-1995;
                                                                                                                                                                        23-JUN-1995;
                                                           09-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vascular endothelial cell growth factor inhibitor; VEGF; sVEGF-RII; KDR; tyrosine-kinase receptor; HUVEC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR was used to construct a truncated form of the KDR gene encoding
603 tegetagtgtgtageeggegetetetttetgeeetgagteeteaggaeeecaagagata
                                                                                                                                                                                                                                      716 gactgtgtcccgcagccgggataacctggctgacccgattccgcgggacaccgctgcagcc
                                                                                                                                                                                                                                                                  868 aagteegtetggeageetggatateeteteetaeeggeaeeeggaaggeeetgeagee
                                                          ----agtececacecteceggtaatgacecegececat
                                                                                      688 tggccgcacgggagagaccctcctccgcccggcccggcatggccccgcctccgc
                                                                                                                                                748 getetagagttteggetecageteceaecetgeaetgagteeegggaeceegggagageg
                                                                                                                                                                             663 agctgtgtttccttagatcgcgcggaccgctacccggcagga-----ctgaaagccca
                                                                                                                                                                                                         808 gtcagtgtgtggtcgctgcgtttcctctgcctgcgccgggcatcacttgcgcgccgcaga
                                                                                                                                                                                                                                                                                              776 g-cggctggagccagggggggggggggggcccgcgcccggtcttgcgctgcgggg---
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1048 cgagttctgggcatttcgcccggctcgaggtgcagg 1083
                                                                                                                                                                                                                                                                                                                                                                                                                  889 tgagaactgggctctgtgcccagcgcgaggtgcagg 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 99-100; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
269..2264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDR truncated sVEGF-RII DNA
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                                                         556 cggacgcaggg-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-316941/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R62486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1994;
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Example 7; Fig 10A-B; 47pp; English.

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                                                                                                                                   cagccgcggctggagccagggcgccggtgccccgctctccccggtcttgcgctgcggg 830
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial cell growth factor; VEGF; receptor; inhibitor; soluble; treatment; angiogenesis; psoriasis; tumour; arthritis;
a truncated, soluble form, sVEGF-RII (R62486), of KDR (amino acids 1-663). sVEGF-RII was expressed in Sf9 cells. It can be used to inhibit VEGF-mediated mitogenesis.
                                                                                                      2;
                                                                            7.6%; Score 70.6; DB 15; Length 2264; Similarity 63.9%; Pred. No. 2.5e-10; 10; Conservative 0; Mismatches 74; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_except= (pos: 263..265, aa: Gln)
/transl_except= (pos: 266..268, aa: Asn)
/product= "truncated VEGF receptor sVEGF-RII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/transl_except= (pos: 260..262, aa: Glu)
                                                                                                                                                                                                                                                                                                                                                                                                       Soluble truncated VEGF receptor (VEGF-RII) encoding DNA.
                                           Sequence 2264 BP; 606 A; 537 C; 569 G; 552 T; 0 other;
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        V09331 standard; DNA; 2264 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0232538
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1994;
                                                                                        Best Local Simi
Matches 140;
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                                                                             Query Match
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growth factor receptor - and related vector and transformed cells, expressing soluble inhibitor of VECF useful for inhibiting angiogenesis, e.g. for treatment of psoriasis, arthritis, tumours

Nucleic acid encoding soluble form of vascular endothelial cell

94US-0232538. 93US-0038769.

21-APR-1994; 25-MAR-1993;

Kendall RL, Thomas KA; (MERI) MERCK & CO INC.

WPI; 1998-120032/11. P-PSDB; W47037.

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5
                                                      This DNA encodes a soluble truncated form of KDR, a vascular endothelial cell growth factor (VEGF). This truncated sVEGF-RII contains the extracellular domain of KDR. A related soluble VEGF receptor/inhibitor (SVEGF-RI) molecule represents a fragment of the VEGF receptor that binds VEGF with high affinity but is unable to transduce a signal. sVEGF-RI is used to inhibit VEGF activity, specifically VEGF-induced angiogenesis, particularly for treatment of psoriasis, rheumatoid arthritis, haemangiomas, angiofilbromas, diabetic retinopathy, neovascular glaucoma or tumour vascularisation. The sVEGF-RI can be administered topically or intravenously or from slow-release matrices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  771 cagccgcggctggagccagggcgccggtgccccgcgctctccccggtcttgcgctgcggg 830
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                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 70.6; DB 19; Length 2264; 63.9%; Pred. No. 2.5e-10; ative 0; Mismatches 74; Indels 5;
                                                                                                                                                                                                                                                                                         Sequence 2264 BP; 606 A; 537 C; 569 G; 552 T; 0 other;
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Job time: 13813 sec
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(without alignments)
1137.715 Million cell updates/sec
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2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/pcTUS_COMB.seq:*
6: /cgn2_6/ptcdata/2/ina/pcTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM nucleic - nucleic search, using sw model
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length: 2000000000
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli		'n	2	m	'n	Sequence 5, Appli	'n	'n	7	'n	2	16,	16,	1, 4	ω,	1	9	Patent No. 5352575	1,	~	Patent No. 5395760	.,	-	Sequence 1, Appli	ì - i	ı,
SUMMARIES	US-08-443-861-1	US-08-193-829B-1	US-07-813-593-3	US-07-977-451-5	US-07-946-507-3	US-08-252-517-5	US-07-906-397A-5	US-08-601-891-5	US-09-021-324-5	PCT-US92-02750-7	PCT-US92-05401-5	PCT-US92-09893-5	US-08-232-538-16	US-08-786-164-16	US-08-586-165-1	US-08-586-165-8	US-09-368-590-1	US-07-975-526-6	5352575-6	US-08-385-229-1	US-08-650-000-1	5395760-1	US-08-477-347-2	US-07-945-283-1	US-09-240-410-1	US-08-118-200-1	US-08-458-745-1
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% Query Match	18.3	18.3	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	7.6	7.6	4.3	4.3	4.3	4.2	4.0	9. 6.	3.9		9.9	3.8	3.7	3.7	3.7
Score	169	9	154.6	154.6	154.6	154.6	154.6	154.6	154.6	154.6	154.6	154.6	9.07	70.6	40	40	40	36	37.4	36	36	36	36	35.4	34.6	34.2	34.2
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LOCATION:

Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli	Sequence 8, Appli
US-08-726-214-1 US-08-076-011-1 US-08-803-23-443B-1 US-08-858-003-29 US-08-99-43-1 US-08-99-43-1 US-08-99-43-1 US-08-99-48-166-29 US-08-99-385A-1 US-09-09-885-5 US-09-09-385A-5 US-09-09-385A-1 US-09-01-385A-5 US-09-01-385A-5 US-09-01-385A-5 US-09-01-385A-1 US-09-01-385A-1 US-09-01-385A-1 US-09-01-385A-1 US-09-01-385A-1 US-08-572-951-3 US-08-572-951-3 US-08-01-01-01-01-01-01-01-01-01-01-01-01-01-	US-09-356-952-8
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Risau, Werner
APPLICANT: Millauer, Birgit
APPLICANT: Gazit, Aviv
APPLICANT: Levitzki, Alex
TITLE OF INVENTION: Fik-1 Is A Receptor For Vascular
TITLE OF INVENTION: Endothelial Growth Factor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,861
FILING DATE: 22-MAY1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/193,829
FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REPERENCYOCKET NUMBER: 36,742
TELECAMUNICATION INFORMATION:
TELECAMICATION NUMBER: 2(212)790-990
TELECAMICATION NUMBER: 2(212)790-990
TELECAMICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5470 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-443-861-1; Sequence 1, Application US/08443861; Patent No. 5851999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
286..4386
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70 GCCCAGACTGTGTCCCGCAGCCGGGATAACCTGGCTGACCCGATTCCGCGGACACCCGCTG 129
                                                                                                                                                                                                                                                                                                                                  830 gggcgcataccgcctctgtgacttctttgcgggccagggacggaaggagtctgtgcct 889
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                                                                                                                                                                                                                                                                                                                                                                            190 GGGC-CATACCGCCTCTGTGACTTCTTTGCGGGCCAGGGACGGAGGAGGAGTCTGTGCCT 248
                                                                                                             4; Gaps
                                                            Score 169; DB 2; Length 5470;
Pred. No. 3.5e-36;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ullrich, Axel
APPLICANT: Risau, Werner
APPLICANT: Risau, Werner
APPLICANT: Millauer, Birgit
APPLICANT: Gazit, Aiv
APPLICANT: Gazit, Alex
TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
TITLE OF INVENTION: Endothelial Growth Factor
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,829B
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                        890 gag-aactgggctctgtgccca-gcgcgaggtgcagg 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 GAGAAACTGGGCTCTGTGCCCAGGCGCGAGGTGCAGG 285
                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7683-060
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08193829B Patent No. 6177401 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5470 base pairs
TYPE: nucleic acid
STRADEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 761
TELECOMMUNICATION INFORMATION:
                                                              18.3%;
98.2%;
                                                              Query Match 18.3%
Best Local Similarity 98.2%
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: 286..4386
US-08-193-829B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-193-829B-1
US-08-443-861-1
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830 gggcgcataccgcctctgtgacttctttgcgggccagggacggaggaggagtctgtgcct 889
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   Length 5470;
18.3%; Score 169; DB 4; Length 547
98.2%; Pred. No. 3.5e-36;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: PECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/813,593
FILING DATE: 19920415
                                                                                                                                                                                                                                                                                                     890 gag-aactgggctctgtgccca-gcgcgaggtgcagg 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19920415
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/07813593 Patent No. 5185438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Query Match 18.39
Best Local Similarity 98.29
Matches 213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
STRANDEDNESS: single
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208..4311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-07-813-593-3
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COMPUTER READABLE FORM:
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                                                                                                                                                        4; Gaps
                                                                                                                                                                                                        16.7%; Score 154.6; DB 1; Length 5406; 96.2%; Pred. No. 2.5e-32; tive 0; Mismatches 4; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Lemischka, Ihor R.

TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL

TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSE: Imclone Systems Incorporated

STREET: 180 Varick Street

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OFTWAILING STSTEM: PC-UOS/MS-DUS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19921119
CLASSIECATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNASSIGNED
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW #1102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 15-APR-1992
PRIOR APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 15-APR-1992
PRIOR APPLICATION NUMBER: US PCT/US92/02750
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/813,593 FILING DATE: 24-DEC-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/793,065 FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-07-977-451-5
Sequence 5, Application US/07977451
; Patent No. 5270458
                                                                                                                                                Matches 201; Conservative
                   mat_peptide
208..4308
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                                                                                                           Query Match
Best Local Similarity
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-07-813-593-3
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60 GGCTGGAGCCAGGGCGCCGGTG-CCCGCGCTCTCCCGGTCTTGCGCTGCGGGGCCCGAT 118
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TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILLING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILLING DATE: 02-APR-1991
ATTORNEY AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                897 gggctctgtgccca-gcgcgaggtgcagg 924
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                                                                                                                                                                              REFERENCE/DOCKET NUMBER: LEM-3-7P
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION CR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/07946507
Patent No. 5283354
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265..4308
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208..264
                                                                                                                                                                                                                                                                                                                                    double
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208..4311
                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: doubl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
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LOCATION:
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; LOCATION:
US-07-977-451-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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CORRESPONDENCE ADDRESS:
                                                                                                         New York
New York
Y: U.S.A.
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                                                                                                                                                                                                                          ZIP: 10014
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FEATURE:
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US-08-252-517-5
                                                                                                                                                                                          COUNTRY:
                                                                                                             CITY:
STATE:
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Best Local Similarity 96.2%; Pred. No. 2.5e-32;
Matches 201; Conservative 0; Mismatches 4; Indels 4;
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                    MEDIJON TIPE: FIDEPY GIST.
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,507
FILING DATE: 19290917
CLASSIFICATION NUMBER: US/07/913,593
FRIDR APPLICATION NUMBER: US/07/813,593
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US/07/93,065
FILING DATE: US/07/191
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,913
FILING DATE: US/07/191
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,913
FILING DATE: US/07/191
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,913
FILING DATE: US/07/728,913
FILING DATE: US/07/728,913
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           897 gggctctgtgccca-gcgcgaggtgcagg 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Feat, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-645-1405
TELEFAX: 212-645-1405
TELEFAX: 212-645-1405
TELEFAX: 212-645-1405
TELEFAX: 212-645-1405
TELEFAX: 212-645-1405
TEREFAX: 212-645-1405
    Floppy disk
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LOCATION: 208..4308
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    MEDIUM TYPE:
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US-07-946-507-3
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ADDRESSEE: Inclone Systems Incorporated
STREET: 180 Vorick Street
CTTT: New YORK
COUNTRY: U.S.A.
COMPUTES: Inclone Systems Incorporated
STATE: New YORK
COUNTRY: U.S.A.
COMPUTES: Inclone Systems
MEDIUM TYTE: Floppy disk
COMPUTES: Inclone Floor Systems
STATE: Bloopy disk
COMPUTES: Inclone Floor Systems
STATE: New YORK
COUNTRY BROOM SYSTEMS: DC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREAN PAPLICATION NATA:
SAPLICATION NUMBER: US 07/977.451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION NUMBER: US 07/977.451
FILING DATE: 26-JUN-1992
PRIOR APPLICATION NUMBER: US 07/977.451
FILING DATE: 26-JUN-1992
PRIOR APPLICATION NUMBER: US 07/977.451
FILING DATE: 26-JUN-1992
PRIOR APPLICATION NUMBER: US 07/97.666
FILING DATE: 26-JUN-1992
PRIOR APPLICATION NUMBER: US 07/793.065
FILING DATE: 15-APR-1992
PRIOR APPLICATION NUMBER: US 07/793.065
FILING DATE: 15-APR-1991
APPLICATION NUMBER: US 07/793.065
APPLICATION NUMBER
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DB 1; Length 5406;

16.7%; Score 154.6;

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FRAGMENT TYPE: N-terminal
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208..4311
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U. ZIP: 10014
                                                                                                                                                               : NAME/KEY:
; LOCATION:
US-07-906-397A-5
                                                                                                   LOCATION:
FEATURE:
                                                                          NAME/KEY:
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US-08-601-891-5
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                                           FEATURE:
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                                           4; Gaps
                                                                                                                         4; Indels
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APPLICANT: Lemischka, Ihor R.

TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE AND THEIR LIGANDS
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAPPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,397A
FILING DATE: 19920626
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION NUMBER: US 07/793,065
FILING DATE: 28-JUN-1991
PRIOR APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION ADATA:
APPLICATION ADATA:
APPLICATION ADATA:
APPLICATION ADATA:
APPLICATION ADATA:
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APPLICATION APPLICATION DATA:
APPLICATION 
   96.2%; Pred. No. 2.5e-32; iive 0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/679,666 FILING DATE: 02-APR-1991 ATTORNEY/AGENT INFORMATION: NAME: Felt, Irving N. REGISTRATION NUMBER: 28,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/07906397A Patent No. 5621090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 96.2
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
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Gaps
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                                                                                 Score 154.6; DB 1; Length 5406;
Pred. No. 2.5e-32;
0; Mismatches 4; Indels 4;
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Patent No. 5747651
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 39-NOV-1992
PRIOR APPLICATION NUMBER: US 07/007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                16.78;
96.28;
                                                                                               Best Local Similarity 96.2
Matches 201; Conservative
mat_peptide 208..4308
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718 ctgtgtcccgcagccgggataacctggctgacccgattccgcgggacaccgctgcagccgc 777
                                              COMPUTER READABLE FORM:
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Best Local Similarity
Matches 201; Conserva
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 New York
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                                                                MEDIUM TYPE:
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                             10014
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COCATION:
US-09-021-324-5
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                 COUNTRY:
 STATE:
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Pred. No. 2.5e-32;
0; Mismatches 4; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: ImClone Systems Incorporated 180 Varick Street
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                                                                                                                                                                              NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                           APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
                              US 07/793,065
                                                                            APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09021324
Patent No. 5912133
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.7%;
96.2%;
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LENGTH: 5406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MODEOULE TYPE: CDNA
HYPOTHETICAL: NO
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
FILING DATE: 24-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal
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Best Local Similarity 96.23
Matches 201; Conservative
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208..264
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265..4308
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ADDRESSEE: Imclone S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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US-08-601-891-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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16.7%; Score 154.6; DB 2; Length 5406; 96.2%; Pred. No. 2.5e-32; tive 0; Mismatches 4; Indels 4;
             COMPUTER: IBM PCFF1 COMPATIBLE
COMPUTER: IBM PCF COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,324
                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION NUMBER: THAN 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
APPLICATION NUMBER: US PCT/US92/02750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PREDICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
RECISTRATION NUMBER: 28,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: LE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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265..4308
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208..264
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60 GGCTGGAGCCAGGGCGCCGGTG-CCCGCGCTCTCCCCGGTCTTGCGCTGCGGGGGCCGAT 118
                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       Sequence 5, Application PC/TUS9205401
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.7%;
Best Local Similarity 96.2%;
Matches 201; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-645-2054 INFORMATION FOR SEQ ID NO: 5:
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LOCATION: 208..4308
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STRANDEDNESS: SINGle
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208..4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
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: U.S.A.
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ZIP: 10014
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PCT-US92-05401-5
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                                                                                                 1 CTGTCTCCCCCAGACCTGGCTGACTGCCGATTCCGCGGACACCCGTGCAGCCGC 59
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                                                                                                                                                                                                                                                                                     APPLICANT: LEMISCHKA, IHOR R.
TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell
TITLE OF INVENTION: Receptors And Their Ligands
NUMBER OF SQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920402
CLASSIFICATION: 435
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Best Local Similarity 96.2%; Pred. No. 2.5e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: FEIT, IRVING N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPPT
REFERENCE/TOCKET NUMBER: LEM-3-PPPPT
TELEPHONE: 212-645-1405
TELEPAK: 212-645-1405
                                                                                                                                                        Sequence 7, Application PC/TUS9202750 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
I-ENGTH: 5406 base pairs
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LOCATION: 208..4308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                           CITY: NEW YORK STATE: NEW YORK
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LOCATION: 208.
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                      10014
                                                                                                                                                                                                                                  RESULT 10
PCT-US92-02750-7
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PCT-US92-02750-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                         SOFTWARES PATENTIN SOLDEN.

SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05401
FILING DATE: 19920626
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Felt, Irving 18,601
REGISTRATION NUMBER: 28,601
REGISTRATION NUMBER: LEM-3-PPPPPT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1005
TELECOMMUNICATION 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 154.6; DB 5;
Pred. No. 2.5e-32;
0; Mismatches 4;
                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
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711 geccagaetgigtecegeageegggataaeetggetgaeeegatteegeggaeaeegetg 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 cagccgcgggtggagccaggggggggggggggggggggttttgcgggtttggggtgggg 830
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119 ACCGCCTCTGTGACTTCTTTGCGGGCCAGGGACGAGAAGGAGTCTGTGCCTGAGAACT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2264;
                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Thomas, Kenneth A.
APPLICANT: Kendall, Richard L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
TITLE OF INVENTION: GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70.6; DB 1; Length 22
Pred. No. 6e-10;
0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               887 cctgagaact-gggctctgtgcccagcgcgaggtgcagg 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 CTCCCGAGTTCCGGCATTTCGCCCGGCTCGAGGTGCAGG 269
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000 126 E Lincoln Avenue
                                       18888IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   Sequence 16, Application US/08232538 Patent No. 5712380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATORNEY TRORMATION:
ATTORNEY AGENT INFORMATION:
NAME: Wallen, John W.III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 1888;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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Best Local Similarity 63.9
Matches 140; Conservative
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 07065-0907
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US-08-786-164-16
                                                                                                                                                                    US-08-232-538-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GGCTGGAGCCAGGGCGCGGTG-CCCGCGCTCTCCCCGGTCTTGCGCTGCGGGGGCCGAT 118
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                                                                                                                                                                Sequence 5, Application PC/TUS9209893
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOFENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09893
FILING DATE: 19921116
CLASSIFICATION:
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Inclone Systems Incorporated
STREET: 180 Variok Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
                                           179 GGGCTCTGTGCCCAGGCGCGAGGTGCAGG 207
                   897 gggctctgtgccca-gcgcgaggtgcagg 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEM-3-7PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY FACENT INFORMATION:
NAME: Feit, Irving N.
REGISTATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-645-1405
TELEFAX: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal
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Best Local Similarity 96.29
Matches 201; Conservative
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208..264
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265..4308
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MEDIUM TYPE: Floppy
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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; LOCATION:
PCT-US92-09893-5
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                                                                                                                                            PCT-US92-09893-5
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LOCATION:
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CCATION:
US-08-586-165-1
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NAME/KEY:
                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GCAGAAAGTCCGTCTGGCAGCCTGGATATCCTCTCCTACCGGCACCCGCAGACGCCCCTG 110
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Sequence 16, Application US/08786164

Patent No. 5861484

GENERAL INFORMATION:

APPLICANT: THOMAS, KENNETH A.

TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL

TITLE OF INVENTION: CELL GROWTH FACTOR

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. BOX 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 CTCCCGAGTTCCGGCATTTCGCCCGGCTCGAGGTGCAGG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                887 cctgagaact-gggctctgtgcccagcgcgaggtgcagg 924
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/786,164
FILING DATE: 21-JAN-1997
FLIASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 1888BDA
TELECOMMUTICATION INFORMATION:
TELEPHONE: 908-594-305
TELEFAX: 908-594-4720
                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08586165
Patent No. 6054298
GENERAL INFORMATION:
APPLICANT: Lanfer, Edward M.
APPLICANT: Orozco, Olivia E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Mark Hand, J
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2264 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
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07065-0900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-586-165-1/c
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..678, 682..687, 691..807, 811..843, 850..870,
874..990, 994..1056, 1060..1083, 1087..1104, 1108
APPLICANT: Tabin, Clifford J.

TILE OF INVENTION: Fringe Proteins and Pattern Formation NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Milita Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.3%; Score 40; DB 3; Length 1120; 51.7%; Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85; Indels
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-JAN-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Job time: 17499 sec
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REPRENCE/DOCKET NUMBER: HU95-
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 51.79
Matches 91; Conservative
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STRANDEDNESS: single
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em_esthum14:*
em_esthum15:*
em_esthum17:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            10228115 seqs, 4726426750 residues
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            US-09-445-201-1_COPY_6036_6959
924
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Maximum Match 100%
Listing first 45 summaries
                                                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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11
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                         em_gss_huml:
em_gss_humd:
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em_gss_rod6:*
em_gss_rod7:*
em_gss_rod8:*
gb_gss35:*
gb_gss35:*
gb_gss37:*
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em_gss_pln2:
em_gss_pro1:
em_gss_rod2:
em_gss_rod3:
em_gss_rod4:
em_gss_rod5:
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                    em_gss_fun:*
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en_htc:*
gb_est107:*
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gb_est109:*
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em_estro21:*
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9b est60:*

9b est60:*

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9b est63:*

9b est65:*

9b est65:*

9b est66:*

9b est66:*

9b est80:*

9b est81:*

9b est100:*

9b est60:*

9b est101:*

9b est101:*
9D_est48...
9D_est48...
9D_est51...
9D_est52...
9D_est54...
9D_est55...
9D_est55...
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AA962730 co899b12.s
AQ937916 NB6-648R
AL054280 Drosophil
AL098842 Drosophil
AL106054 Prosophil
BP983618 602304736
AW0026648 wu60902.x
AQ93893 NL1-BL13R
AL05652 Drosophil
BF203166 601866196
AL101954 Prosophil
BF203166 601866196
AL101954 Drosophil
BF800542 963016406
AL065629 Drosophil
BF806042 963016406
AL065629 Drosophil
BF806042 963016406
AL065629 Drosophil
BF806060 602093786
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AG013041 Home sapi
AL062395 Drosophil
AL054280 Drosophil
AL01858 Drosophil
AL01858 Drosophil
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AL056542 Drosophil
AL05642 Drosophil
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AL589555 DKFZp451M
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AL053013 Drosophil
AL101589 Drosophil
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NIH-MGC http://mgc.ncl.nih.gov/.
Natlonal Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602110935F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4238984 5', mRNA sequence.
                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL107269
AL050923
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AZ186391
                                                                BF543874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                              CNS0072Q
CNS017SY
AA962730
                                                                                                                                                                                                                                                                                                   AQ937916
CNS004NB
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CNS010EW
                                                            BE543874
BB593727
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Query
Match Length DB
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    REAL PROPERTY

    REAL PROPERTY
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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           No.
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/ .763
/ Organism="Musculus"
/ Organism="Musculus"
/ Organism="Musculus"
/ Ob_xref="taxon:10090"
/ Clone="InAGE:4238984"
/ Clone="InAGE:4238984"
/ Clone="InAGE:4238984"
/ InD_Lost="NCI_CGAP_Kid14"
/ InD_Lost="DiltOB (T1 phage-resistant)"
/ Note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
56 a 218 c 223 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 192).
Alzawa,K., Akahira,S., Akimura,T., Arai,A., Arakwa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojina,Y., Konno, W.H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,Y., Yoshidi,A., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB597428 RIKEN full-length enriched, 12 days embryo spinal cord Mus musculus CDNA clone C530002A01 5', mRNA sequence.
BB597428.1 GT:11506029
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.t column: 09
High quality sequence stop: 657.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666 tgtgtttccttagatcgcgcggaccgctacccggcaggactgaaagcccagactgtgtcc 725
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Matches 255; Conservative
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182 CGCTCTGTGGG 192

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Email: genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninci,P. Nishiyama,Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Rawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463, 403, 1999)
Carninci,P., and Hayashizaki,Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand oDNA was
primed with a primer [5]
                                                                                                                                                                                                                                 The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="C530002A01"
/clone_lib="RIKEN full-length enriched, 12 days embryo spinal cord"
//tissue_type="spinal cord"
RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
Unpublished (2000)
Context: Yoshinide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 700 caggactgaaagcccagactgtgtcccgcagccgggataacctggctgacccgattccgc 759
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/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 161; Length 192;
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                                                                                                                                                                                                                                                                                                                            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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Pred. No. 2.6e-33;
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820 tgcgctgcggg 830

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/note-"Vector: pTT7D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day embryos, after a series of subtractions to reduce the representation of Connas from which ESTS had already been generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2P, UI-R-C), UI-R-C0, UI-R-A1, UI-R-E1. The tag is a siring of 3-5 nucleotides present between the Not I site and the oligo-df track whichallows identification of the library of origin of a clone within themixture. The subtracted library of origin of a clone within themixture. The subtracted library of origin of a clone within themixture in a hybridization with the UI-R-C3 was constructed as follows: PCRamplified been derived was used as a driver in a hybridization with the UI-R-C2P library in the form of single-stranded circles and electroporated into DH10B bacteria (lifeTechnologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-866, 1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: msoares@blue.weeg.ulowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1785489
Seq primer: M13 Forward.
Location/Qualifiers
                                                                                                                                                                                                                                                      Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, M.F., \ Lennon, G. \ and \ Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 9250
Fax: 319 335 9565
                                                      11-DEC-2000
                                                             BF543874 207 bp mRNA EST 11-DEC-2000
UI-R-C3-tg-c-12-0-UI.rl UI-R-C3 Rattus norvegicus cDNA clone
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/db_xref="taxon:10116"
/clone="U1-R-C3-tg-c-12-0-UI"
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/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Program for Rat Gene Discovery and Mapping
                                                                                                      UI-R-C3-tg-c-12-0-UI 5', mRNA sequence. BF543874
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97044477
Contact: Soares, MB
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MEDLINE
COMMENT
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TITLE
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RESULT
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'db_xref="taxon:10090"

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ISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 193)

Alzawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hangafaki,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Hiraoka,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Miszaki,A., Nakanura,M., Nakanura,M., Nishi,K., Sakai,K., Sakai,R., Sato,K., Shibata,Y., Shinaqawa,A., Shiraki,T., Sogabe,Y., Sato,K., Shibata,Y., Shinaqawa,A., Shiraki,T., Waramatsu,M. and Hayashizaki,Y. Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yamamatsu,M. and Hayashizaki,Y. Wasunishi,A., Viramamatsu,M. and Hayashizaki,Y. Wasunishi,A., Yasunishi,A., Waramatsu,M. and Hayashizaki,Y. Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
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URL:http://genome.rtc.riken.go.jp,
Carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehatose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparation System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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        DB 150; Length 207;
                                                            23; Indels
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
  16.4%; Score 151.2; DB 1
88.0%; Pred. No. 1.4e-31;
iive 0; Mismatches 23
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Query Match 16.4
Best Local Similarity 88.0
Matches 176; Conservative
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/organism="Mus musculus"

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AL589555 335 bp mRNA EST 07-MAR-2001
DKF22p451M0219_r1 451 (synonym: hlccl) spinal cord Homo sapiens cDNA
Clone DKF2p451M0219 5', mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
          /clone_lib="RIKEN full-length enriched, 4 days neonate male adipose"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                                                                                                                                                                                                          Score 146.2; DB 1
Pred. No. 3.5e-30;
0; Mismatches 28
                                                                                                                                                                                                                                                                                           29 t
                                                          /dev_stage="4 days neonate"
/lab_host="DH10B"
                                             /tissue_type="adipose"
                                                                                                                                                                                                                                                                                           82 g
/clone="B430204G23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL589555.1 GI:13243327
                                                                                                                                                                                                                                                                                                                                          15.8%;
85.3%;
                                   /sex="male"
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Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :

Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :

Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Droscophila Genome Project (BDCP).

The BDCP is constructing a physical map of the Droscophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Droscophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Centelics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                       sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19016 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                 This clone (DKFZp451M0219) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               711 geccagaetgtgteeegeageegggataacetggetgaeeeggatteegeggaeaeegetg 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 771 cagccgcggctggagccaggggcgccggtgcccggctctccccggtcttgcgctgcgg 830
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
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108 g 59 t
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                                                                                                                                                                                                                                                                                          /clone="DKFZP451M0219"
/clone_lib="451 (synonym: hlcc1) spinal cord"
/tissue_type="human spinal cord"
/dev_stage="human spinal cord"
/dev_stage="human"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.6%; Score 79.2; DB 1
Best Local Similarity 66.4%; Pred. No. 2e-11;
Matches 146; Conservative 0; Mismatches 6
                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                               No s1 sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector:
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Direct Submission
Submitted (O2-JUW-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xxef="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19DI6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%; Score 62; DB 219;
14.0%; Pred. No. 1.5e-06;
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://pacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN08C07 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 tecaccagaaaccgagetgcgtecagatttgeteteagatgcgaettgecgceggeaca 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    883 TSSMSSSSBSSSSGSSSSGTSSACVKCNASSSCGCCGCGMABCCMCSSSSSCCGSASA 824
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                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="texon:7227"
/clone_lib="RPCI-98"
/clone="BACRI9D16"
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COMMENT

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http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Geneyieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 gcagcaagtgtctcagagcccattactggctacattttacttccaccagaaaccgagctg 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 GGGGNNNNNGGNNNTTNNTNGGTTTNNNGGNNNNNSCCCSNCTNCNNNNTNTTNSSSSSS 215
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila,
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/plasmid="pBelobAC11"
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/clone="BACN08C07"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Homo sapiens genomic DNA, 21q region, clone: 72018SpN42, genomic survey sequence.
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/db_xref="taxon:7227"
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                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                    Submitted (25-AUG-1998) to the DDBJ/EMBL/GenBank databases. Massalira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Saqamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
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Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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On Feb 5, 1999 this sequence version replaced gi:2913972.
AG005396: Submitted (26-Feb-1998).
Location/Qualifiers
                                                                                           1 (bases 1 to 920)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1998) In press
2 (bases 1 to 920)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
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Pred. No. 0.012;
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/clone="72018SpN42"
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AUTHORS JOURNAL

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**Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://warpac.med.bDfffalo.edu/drosophila_bac.htm.
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                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                  - Web: www.genoscope.cns.fr.
- Web: www.genoscope.cns.fr.
- Web: www.genoscope.cns.fr.
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovy Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Localion/Quallifiers

S Localion/Quallifiers
                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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Submitted (02-JUW-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fultfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecord ingestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.thm.
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/db_xref="taxon:7227"
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RESULT 14

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d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web: www.genoscope.com.fr)
Determination of this BAC-end sequence was carried out as part of
Determination of this BAC-end sequence was carried out as part of
Determination with the European Drosophila Genome Project (EDGP)
thtp://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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               Drosophila melanogaster genome survey sequence T7 end of BAC BACNO8K01 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL101858
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
26-JUL-1999
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Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
[ (bases 1 to 1101)
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/plasmid="pBeloBAC11"
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/clone_lib="DrosBAC"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila enome Project (BDGP).

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                                                                    Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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4.8%; Score 44.8; DB 219; Length 935;
Best Local Similarity 28.3%; Pred. No. 0.097;
Matches 108; Conservative 94; Mismatches 179; Indels 1;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 935)
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Search completed: June 21, 2001, 15:34:07 Job time: 7651 sec ,